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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 23, 2003, 14:08:00 ; Search time 4200.2 Seconds

(without alignments)
2746.659 Million cell updates/sec

Title: US-09-856-320A-2

Perfect score: 1523

Sequence: 1 MGRRLRLRDMKSSGRLTNA.....GYTVKCKVVDIMQETMKNN 282

Scoring table:

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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 2888711 segs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1523	100.0	1106	6	AX016287 Sequence
2	1523	100.0	1106	6	BD137019 Human CAS
3	1523	100.0	1158	6	AX016289 Sequence
4	1523	100.0	1158	6	BD137020 Human CAS
5	1523	100.0	1186	9	AB012817 Homo sapi
6	1523	100.0	1204	6	AX358932 Sequence
7	1523	100.0	1204	6	AX362425 Sequence
8	1523	100.0	1204	6	AX454622 Sequence
9	1523	100.0	1204	6	AX464372 Sequence
10	1523	100.0	1204	6	AX491100 Sequence
11	1523	100.0	1204	6	AX697101 Sequence
12	1523	100.0	1301	6	BD091587 Novel ser
13	1523	100.0	1301	6	AB041036 Homo sapi
14	1523	100.0	1314	6	AR098430 Sequence
15	1523	100.0	1314	6	BD130920 Serine pr
16	1411	92.6	1181	9	AB013730 Homo sapi
17	1411	92.6	1213	9	BC022068 Homo sapi
18	1410	92.6	1192	6	AR152173 Sequence
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20	1388.5	91.2	930	9	AB078780 Homo sapi
21	1388.5	91.2	934	6	BD091589 Novel ser
22	1380	90.6	1191	6	BD139483 Extended
23	1279.5	84.0	1164	6	AX661915 Sequence
24	1233	81.0	833	6	AR060847 Sequence
25	1233	81.0	833	6	BD082136 Novel pro
26	1227	80.6	1052	6	AR219287 Sequence
27	1187	77.9	1256	10	AB016227 Mus muscu
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29	1164	76.4	1213	10	AB016226 Mus muscu
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35	948.5	62.3	200792	2	AC130782 Pan trogl
36	943.5	62.0	176647	2	AC130188 Papio anu
37	916.5	60.2	618	6	AR263825 Sequence
38	817.5	53.7	226890	2	AC135541 Rattus no
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41	739	48.5	472	6	AR263958 Sequence
42	708.5	46.5	974	10	RRAS641 Rattus ra
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RESULT 1

ALIGNMENTS

AX016287 1106 bp DNA linear PAT 07-SEP-2000

LOCUS AX016287

DEFINITION Sequence 1 from Patent WO949055.

ACCESSION AX016287

VERSION AX016287.1 GI:10041854

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Bruck C.E., Coche T., Cassart J.P. and Vinals-Bassols C.

AUTHORS Human casp12 polypeptide, a serine protease

JOURNAL Patent: WO 949055-A 1 30-SEP-1999;

COCHE THIERRY (BE); CASSART JEAN POL (BE); VINALS BASSOLS CARLOTTA (BE)

FEATURES

source 1..1106

Location/Qualifiers

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

BASE COUNT 247 a 348 c 287 g 224 t

ORIGIN

Alignment Scores:

Pred. No.: 6.05e-113 Length: 1106

Score: 1523.00 Matches: 282

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-09-856-320A-2 (1-282) x AX016287 (1-1106)

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QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleu 40

DB 74 AAGGAACCTGGGGCCCGCTCTCCCTCCAGCCATGAGATTCTGAGTTATCTCTG 133

QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyIuThrArgIleIleLysGlyPheGlyLys 60

DB 124 CTGCTCTGGCAACAGGGCTGTGAGGGGAGAGACAGATCATCAAGGGTTCCAGTGC 193

QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlyLysThrArgLeuLeuLysGly 80

DB 194 AAGCTCTACTCCCAAGCCCTGGGACGACGCCCTGTTGAGAGACCGGGCTACTCTGTGG 253

QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100

DB 254 GCGACGCTCATGCCCCCAGATGGCTCTGACAGACGCCACTGCTCAAGCCCCGCTAC 313

QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlyGlyGlyGlyGlnThrArgThr 120

DB 314 ATAGTTTCACTGGGGCAGACAACTCCAGAGGAGGGGTGTGAGCAGACCCGAGCA 373

QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140

DB 374 GGCACCTGAGTCTTCTCCCAAGCCCGGCTTCAACAAAGCTTCCCAACAAACCAAGCCG 433

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QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200

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QY 201 IleGluHisGlnLysCysGluAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220

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RESULT 2

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LOCUS BD137019

DEFINITION Human CASB 12 polypeptide, a serine protease.

ACCESSION BD137019

VERSION BD137019.1 GI:32321964

KEYWORDS JP 2002507425-A/1.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Bruck C.E.M., Cassart J.P., Coche T. and Bassols C.V.

AUTHORS Human CASB 12 polypeptide, a serine protease

JOURNAL Patent: JP 2002507425-A 1 12-MAR-2002;

SMITHKLIN BECHAM BIOLOGICALS SA

COMMENT

OS Homo sapiens (human)

PN JP 2002507425-A/1

PD 12-MAR-2002

PF 17-MAR-1999 JP 2000538015

PR 20-MAR-1998 GB 9806095.7

PI CLAUDINE ELVIRE MARIE BRUCK, JEAN POL CASSART, THIERRY COCHE, PI CARLOTTA VINALS BASSOLS

PC C12N15/09, A61K31/70, A61K38/00, A61P35/00, A61P37/02, C07K16/40, PC C12N1/15,

PC C12N1/19, C12N1/21, C12N5/10, C12N9/64, C12P21/02, C12Q1/02, C12Q1/ PC 68, G01N33/15,

PC G01N33/50, G01N33/50, G01N33/574, G01N33/68, C12N15/00, A61K37/02, PC C12N5/00

CC Human CASB 12 polypeptide, a serine protease. FH Key

FT Location/Qualifiers

FT source 1..1106

Location/Qualifiers

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/mol_type="genomic DNA"

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BASE COUNT 247 a 348 c 287 g 224 t

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Alignment Scores:

Pred. No.: 6.05e-113 Length: 1106

Score: 1523.00 Matches: 282

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

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US-09-856-320A-2 (1-282) x BD137019 (1-1106)

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Db 854 AACCAAT 859

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ACCESSION AX016289
VERSION AX016289.1 GI:10041855
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Bruck,C.E., Coche,T., Cassart,J.P. and Vinals-Bassols,C.

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TITLE Human casb12 polypeptide, a serine protease
JOURNAL Patent: WO 9949055-A 3 30-SEP-1999;
BRUCK CLAUDE ELVIRE MARIE (BE); SMITHKLINE BEECHAM (BE);
COCHE THIERRY (BE); CASSART JEAN FOL (BE); VINALS-BASSOLS CARLOTTA
(BE)
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Qy 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgLleLeuGlnLeuLleu 40
Db 144 AAGGAACCTGGGGCCGCTCTCCCTCCAGGCATGAGATCTGCAGTTAACTCG 203
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Db 204 CTTCCTCTGCAACAGAGGCTTGTAGGGAGAGACAGATCATCAAGGGGTTTCAGTGC 263
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Qy 141 AsnAspIleMetLeuValLysMetAlaSerProValSerLleThrTrpAlaValArgPro 160
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DEFINITION			Human CASB 12 polypeptide, a serine protease.	
ACCESSION			BD137020	
VERSION			BD137020.1 GI:23231965	
KEYWORDS			JP 2002507425-A/2.	
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AUTHORS			Bruck,C.E.M., Caessart,J.P., Coche,T. and Bassols,C.V.	
TITLE			Human CASB 12 polypeptide, a serine protease	
JOURNAL			Patent: JP 2002507425-A 2 12-MAR-2002;	
			SMITHKLINE BEECHAM BIOLOGICALS SA	
COMMENT			OS Homo sapiens (human)	
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			PR 20-MAR-1998 GB 9806095.7	
			PI CLAUDE ELVIRE MARIE BRUCK,JEAN POL CASSART,THIERRY COCHE, P	
			CARLOTA VINALS BASSOLS	
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Db		204	CTTGCTCTGGCAACGAGGGCTTGTAGGGGGAAGACACAGATCATCAAGGGGTTGAGTGC	263

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QY	81	AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr	100
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QY	101	IleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlyGlyCysGluGlnThrArgThr	120
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QY	121	AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg	140
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QY	141	AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro	160
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QY	161	LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTyrTrpGly	180
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QY	181	SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle	200
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QY	201	IleGlnHisGlnLysCysGluAsnAlaTyrProGlyAsnIleThrAspThrMetValCys	220
Db	684	ATTGAGCACCGAAGTGTGTGAAGACGCTTACCCCGGCACATCACAGACCATGTGTGT	743
QY	221	AlaSerValGlnGluGlyGlyLysAspSerCysGlnGlyAspSerGlyGlyProLeuVal	240
Db	744	GCCAGCGTCGACGAAGGGGGGACAGACTCTCCGACAGGGTGACTCGGGGGCCCTCTGGTC	803
QY	241	CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg	260
Db	804	TGTAAACCAAGTCTCTTCAAGGCATTATCTCTCGGGGCGCAGGATCCGTGTGCATCACCCGA	863
QY	261	LysProGlyValTyrThrLysValCysLeuTyrValAspTrpIleGlnGluThrMetLys	280
Db	864	AAAGCTGTGTCTTACAGAAAGTCTGCMAATATGTGACTGTGATTCAGAGACCATGAG	923
QY	281	AsnAsn 282	
Db	924	AAACAT 929	
RESULT 5			
LOCUS	AB012917	1186 bp	mRNA linear PRI 31-JAN-2003
DEFINITION	Homo sapiens mRNA for serine protease (TLSP), complete cds.		
ACCESSION	AB012917		
VERSION	AB012917.1	GI:3649790	
KEYWORDS	TLSP; serine protease (TLSP).		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia; Eutheria: Primates: Catarrhini; Homnidae; Homo.		
AUTHORS	Yoshida,S., Taniguchi,M., Suemoto,T., Oka,T., He,X. and Shiosaka,S		
TITLE	CDNA Cloning and expression of a novel serine protease, TLSP		
JOURNAL	Biochim. Biophys. Acta 1399 (2-3), 225-228 (1998)		
MEDLINE	98438738		
PUBMED	9765601		
REFERENCE	2 (bases 1 to 1186)		
AUTHORS	Yoshida,S.		
TITLE	Direct Submission		
JOURNAL	Submitted (10-APR-1998) Shigetaka Yoshida, Department of Anatomy 1, Asahikawa Medical College; Midorigaoka higashi 2-1-1, Asahikawa, Hokkaido 078-8510, Japan (E-mail: syoshida@asahikawa-med.ac.jp, Tel:81-16-68-2300, Fax:81-16-68-2309)		
FEATURES	Location/Qualifiers		


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Best Local Similarity: 100.00% Mismatches: 0
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QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyLeuThrArgLleLeuGlyPheGlyCys 60
DB 146 CTGGCTCTGGCAACAGGGCTGTAGGGGAGAGACAGAGTATCAAGGGTTCCAGTCC 205
QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlyLysThrArgLeuLeuCysGly 80
DB 206 AAGCTTCACTCCAGCCTGGCAGGAGCCTGTTGAGAGACGCGCTACTCTGTGG 265
QY 81 AlaThrLeuLleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTrp 100
DB 266 GGCAGCCTCATGCCCCCGAGATGGCTCTGACAGCAGCCACTGCTTCAAGCCCGCTAC 325
QY 101 lleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlyCysGluGlnThrArgThr 120
DB 326 ATAGTTCACTGGGGAGCACAACCTCCAGAGAGAGAGGGGTGTAGCAGACCCGGAGA 385
QY 121 AlaThrGlnSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
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QY 141 AsnAspLleMetLeuValLysMetAlaSerProValSerLleThrTrpAlaValArgPro 160
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DB 506 CTCACCTCTCTCCACAGCTGTGTCACTGTGGAGCAGCAGCTTATTTCCGGCTGGGG 565
QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnLleThrLle 200
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DB 686 GCAGAGCTCAGGAAGGGGCAAGAGACTCTCTGCAGAGTGACTCCGGGGCCCTGTGTC 745
QY 241 CysAsnGlnSerLeuGlnLysLleLeuSerTrpGlyGlnAspProCysAlaLleThrArg 260
DB 746 TGTAAACAGTCTCTTCAAGGCAATATCTCTGGGGCAGAGTCCGTGTGATCACCCGA 805
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QY 281 AsnAsn 282
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LOCUS AX358932 1204 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 185 from Patent WO0193983.
ACCESSION AX358932
VERSION AX358932.1 GI:16675367
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
Watnabe,C.K. and Wood,W.I.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0193983-A 185 13-DEC-2001;
Genentech Inc. (US)
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Pred. No.: 6,64e-113 Length: 1204
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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DB 10 ATGCAGAGGTGAGGAGGCTGCGGAGATGAGTATCGGAGAGGTCTCAGCAGCAGC 69
QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgLleLeuGlnLeuLeu 40
DB 70 AAGGAACCTGGGGCCCGCTCTCTCCCGCAGGCCATGAGGATTCTGAGTTAACTCTG 129
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyLeuThrArgLleLeuGlyPheGlyCys 60
DB 130 CTGGCTCTGGCAACAGGGCTGTAGGGGAGAGACAGAGTATCAAGGGTTCCAGTCC 189
QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlyLysThrArgLeuLeuCysGly 80
DB 190 AAGCTTCACTCCAGCCTGGAGGAGCAGCCTGTTGAGAGAGACCGGCTACTCTGTGG 249

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 QY 101 ILeValHisLeuGlyGlnHisAsnLeuGlnLysGlnGluGlyCysGlnGlnThrArgThr 120
 DB 310 ATAGTTACCTGGGGGAGCACAACCTCCAGAAAGAGAGAGGGCTGTGAGCAGACCCGGACA 369
 QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
 DB 370 GGCACGAGTCTCTCCCGCACCCCGCTTCAACAACAGCTCCCGCAACAACACACCGCC 429
 QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
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 QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
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 QY 201 ILeGluHisGlnLysCysGluAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220
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 QY 221 AlaSerValGlnGlnGlyLysAspSerCysGlnGlyAspSerGlyValProLeuVal 240
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 DB 850 AACAAAT 855

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 DEFINITION Sequence 185 from Patent WO0208288.
 ACCESSION AX362425
 VERSION AX362425.1 GI:18694670
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 Baker,K.P., Desnoyers,L., Geritsen,M.E., Goddard,A.,
 Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
 Watanabe,C.K. and Wood,W.I.
 Secreted and transmembrane polypeptides and nucleic acids encoding
 the same
 Patent: WO 0208288-A 185 31-JAN-2002;
 Genentech, Inc. (US)

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Alignment Scores: 6,64e-113 Length: 1204
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 QY 281 AsnAsn 282
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 DEFINITION Sequence 207 from Patent WO0208284.
 ACCESSION AX454622

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VERSION      AX454622.1  GI:21713935
KEYWORDS
SOURCE       Homo sapiens (human)
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS      1 Baker, K.P., Ferrara, N., Gerber, H., Gertsen, M.E., Goddard, A.,
              Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
              Pooni, N.F., Stephen, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
              and Ye, W.
TITLE        Compositions and methods for the diagnosis and treatment of
              disorders involving angiogenesis
JOURNAL      Patent: WO 0208284-A 207 31-JAN-2002;
              Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone
              (US) ; Gerber, Hanspeter (US) ; Gertsen, Mary E. (US) ; Goddard,
              Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
              Hillan, Kenneth J. (US) ; Marsters, Scott A. (US) ; Pan, James (US)
              ; Pooni, Nicholas F. (US) ; Stephen, Jean-Philippe F. (US) ;
              Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William
              I. (US)
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QY      41 LeuAlaLeuAlaThrGlyLeuValGlyGlyIuThrArgIleIleYsgIyPheGluCys 60
DB      130 CTGGCTCTGGCAACAGAGCTTGTAGGGGAGAGACAGAGATCATCAAGGGTTCCAGTCC 189
QY      61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGluLysThrArgLeuLeuCysGly 80
DB      190 AAGCTCATCTCCAGCCCTGGAGGAGCGCTGTTCGAGAAAGCGGGCTACTCTGTGG 249
QY      81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTrp 100
DB      250 GCGAGGCTCATGCCCCCGAGATGGCTCTTCAACAGCAGCCACTGCTCAAGCCCGCTAC 309
QY      101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlyCysGlyGlnThrArgTrp 120
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QY      121 AlaThrGluSerPheProHisSerProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
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QY      201 IleGlnHisGlnLysCysGlnLeuAsnAlaTrpProGlyAsnIleThrAspThrMetValCys 220
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QY      221 AlaSerValGlnGlyGlyLysAspSerCysGlnGlyAspSerGlyGlyProLeuVal 240
DB      670 GCAGGCTCAGAGAGAGGGGCAAGAGCTCCTCGCAGGAGTGAATCCGGGGCCCTCTGTC 729
QY      241 CysAsnGlnSerLeuGlnGlnLysIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
DB      730 TGTAAACAATCTCTCTCAAGGATTAATCTCTCGGGGCGAGATTCGGTGTGATCACCCGA 789
QY      261 LysProGlyValIuThrLysValCysLysTrpValAspTrpIleGlnGlnThrMetLys 280
DB      790 AAGCTGTGTCTTACAGAAAGTGTGCAATATGTGACTGGATCCAGAGAGATGAAG 849
QY      281 AsnAsn 282
DB      850 AACCAAT 855
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AX464372
LOCUS        Sequence 505 from Patent WO0140466.
DEFINITION   AX464372
ACCESSION    AX464372.1  GI:21899202
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens (human)
REFERENCE
AUTHORS      1 Baker, K.P., Beresini, M., DeForge, L., Desnoyers, L., Filvaroff, E.,
              Gao, W.-Q., Gertsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L.,
              Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K.,
              Wood, W.I. and Zhang, Z.
              Secreted and transmembrane polypeptides and nucleic acids encoding
              same
JOURNAL      Patent: WO 0140466-A 505 07-JUN-2001;
              Genentech Inc. (US)
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              /mol_type="genomic DNA"
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BASE COUNT   306 a 364 c 294 g 240 t
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Alignment Scores:
Pred. No.:   6.64e-113      Length:      1204
Score:       1523.00        Matches:      282
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 100.00%        Indels:      0
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QY      21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleuGlnLeuIleu 40
DB      70 AAGGAACCTGGGGCCCGCTCTCTCCCTCCAGGCCATAGAGATTGCAATTAAATCTCG 129
QY      41 LeuAlaLeuAlaThrGlyLeuValGlyGlyIuThrArgIleIleYsgIyPheGluCys 60

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Db      190 AAGCTCACTCCAGCCCTGGCAGGAGCCCTGTTGAGAAAGACCGGGTACTTGTGGG 249
Oy      81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
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Oy      101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlyCysGlyGlnThrArgThr 120
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Oy      141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
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Db      490 CTCACCTCTCTCTACGCTGTCTACTGTCGACACAGCTGCTCATTTCCGGCTGGGGC 549
Oy      181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
Db      550 AGCAGCTCAGGCCCCAGCTTACGCTGCTCAGCTTGCATGCGCCAAATCAATCCATC 609
Oy      201 IleGluHisGlnLysCysGluAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220
Db      610 ATTGGACACCAAAATGTGAAAGCCCAACCCCGCAACATCAAGAACATGTGTGT 669
Oy      221 AlaSerValGlnGlnGlyGlyLysAspSerCysGlnGlyAspSerGlyGlyProLeuVal 240
Db      670 GCCAGCTGACAGAAAGGGGGCAGAGATCTCTCCAGGGTACTCCGGGGCCCTTGTGTC 729
Oy      241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
Db      730 TGTAAACAGTCTCTTCAAGGACATTAATCTCTGGGGCCAGATCCGTGTGCGATCAACCGA 789
Oy      261 LysProGlyValTyrThrLysValCysLysTyrValAspTrpIleGlnGluThrMetLys 280
Db      790 AAGCTGTGTGTACAGAAAGTGTGCAAAATATGTGACTGTGATCCAGAGACGATGAAG 849
Oy      281 AsnAsn 282
Db      850 AACAAAT 855

RESULT 10
AX491100      1204 bp      DNA      linear      PAT 16-AUG-2002
LOCUS      AX491100
DEFINITION      Sequence 207 from Patent WO0200690.
ACCESSION      AX491100
VERSION      AX491100.1 GI:22323887
KEYWORDS
ORGANISM      Homo sapiens (human)
SOURCE      Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
  Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
  Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
  and Ye, W.
  Compositions and methods for the diagnosis and treatment of
  disorders involving angiogenesis
  Patent: WO 0200690-A 207 03-JAN-2002;
  Genentech, Inc. (US)
  Location/Qualifiers
1..1204
FEATURES
source

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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT      306 a      364 c      294 g      240 t
ORIGIN
Alignment Scores:
Pred. No.:      6.64e-113      Length:      1204
Score:      1523.00      Matches:      282
Percent Similarity:      100.00%      Conservative:      0
Best Local Similarity:      100.00%      Mismatches:      0
Query Match:      100.00%      Indels:      0
DB:      6      Gaps:      0
US-09-856-320A-2 (1-282) x AX491100 (1-1204)
Oy      1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaAla 20
Db      10 ATGAGAGAGTTGAGGTGGCTCGGGACTGGAAGTCATCGGCAGAGGTCTCACAGACACC 69
Oy      21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleLeu 40
Db      70 AAGGAACCTGGGGCCCGCTCCCTCCAGGCCCATGAGGATTTCTGCACTTAATCTTG 129
Oy      41 LeuAlaLeuAlaThrGlyLeuValGlyGlyLthrArgIleIleLysGlyPheGluCys 60
Db      130 CTTGCTGGCAACAGGGCTGTGAGGGGAGAGACAGGATCATCAAGGGGTTCAGATGC 189
Oy      61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGluValThrArgLeuLeuGly 80
Db      190 AAGCTCACTCCAGCCCTGGCAGACAGCCCTGTTCAGAAAGACCGGCTACTGTGGG 249
Oy      250 GCGAGCTCATGCCGCCAGATGGCTCTGACACACAGCCCACTGCTCAACCCCGCTAC 309
Db      101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlyCysGlyGlnThrArgThr 120
Oy      310 ATAGTTCACCTGGGGCAGACAACTCCAGAAAGAGAGGGCTGTGAGCAACCCGGACA 369
Db      121 AlaThrGlnSerPheProHisSerProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
Oy      370 GCCACTGAGTCTCTCCCAACCCCGGCTTCAACACAGCTCCCAACAAAGACCAACCGC 429
Db      141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
Oy      430 AATGACATCATGCTGTGTAAGATGACATCGCCAGTCTCCATCACCTGGGCTGTGCGACC 489
Db      161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
Oy      490 CTCACCTCTCTCTACGCTGTGTCTACTGTCGACACAGCTGCTCATTTCCGGCTGGGGC 549
Db      181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
Oy      550 AGCAGCTGACAGCCCGCAAGTTACGCTGCTCAACACCTGCGATGCGCAACATCAACATC 609
Db      201 IleGluHisGlnLysCysGluAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220
Oy      610 ATTGAGACCCAGAAAGTGTGAAAGCCCTACCCCGCAACATCAACAGACACCATGTTGT 669
Db      221 AlaSerValGlnGlnGlyGlyLysAspSerCysGlnGlyAspSerGlyGlyProLeuVal 240
Oy      670 GCCAGCTGACAGAAAGGGGGCAGAGATCTCTGCGAGGTGACTCCGGGGCCCTTGTGTC 729
Db      241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
Oy      730 TGTAAACAGTCTCTTCAAGGACATTAATCTCTGGGGCCAGAGATCCTGTGCGATCAACCGA 789
Db      261 LysProGlyValTyrThrLysValCysLysTyrValAspTrpIleGlnGluThrMetLys 280
Oy      790 AAGCTGTGTGTACAGAAAGTGTGCAAAATATGTGACTGTGATCCAGAGACGATGAAG 849
Db      281 AsnAsn 282

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Db      850 AACAA 855
RESULT 11
LOCUS   AX697101      1204 bp      DNA      linear      PAT 02-APR-2003
DEFINITION
Sequence 169 from Patent WO0078961.
ACCESSION
AX697101
VERSION
AX697101.1 GI:29498066
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1
AUTHORS
Ferrara,N., Stewart,T.A., Williams,P.M., Baker,K.P., Desnuyers,L.,
Eaton,D.L., Gao,W.Q., Pan,J., Botstein,D., Fong,S., Goddard,A.,
Godowski,P.J., Gutney,A.L., Smith,V., Tuma,D., Wood,W.I.,
Grimaldi,C.J., Hillan,K.J., Paoni,N.F., Roy,M.A. and Watanabe,C.K.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL
Patent: WO 0078961-A 169 28-DEC-2000;
Genentech Inc. (US)
FEATURES
source
1..1204
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT      306 a      364 c      294 g      240 t
ORIGIN
Alignment Scores:
Pred. No.:      6,64e-113      Length:      1204
Score:      1523.00      Matches:      282
Percent Similarity:      100.00%      Conservative:      0
Best Local Similarity:      100.00%      Mismatches:      0
Query Match:      100.00%      Indels:      0
DB:      Gaps:      0
US-09-856-320A-2 (1-282) x AX697101 (1-1204)
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QY      21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgLLeuGlnLeuLeu 40
Db      70 AAGGAACCTGGGGCCGCTCTCCCTCCAGGCGCATGAGATTCTGCAGTTAATCTG 129
QY      41 LeuAlaLeuAlaThrGlyLeuValGlyGlyLeuThrArgLLeuLeuGlyPheGlyLys 60
Db      130 CTTCCTCTGGCAACAGGGCTTTGAGGGAGAGACCAAGATCATCAAGGGGTTCCAGTGC 189
QY      61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlyLysThrArgLeuLeuGly 80
Db      190 AAGCCTCAGCTCCAGGCTGGGAGGAGCGCTTTGAGAGAGCGGCTACTCTGTGG 249
QY      81 AlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
Db      250 GCGACGCTCATGCGCCCGCAGATGGCTCTGAGAGCGACGCCACAGCTCAAGCCCGCTAC 309
QY      101 ILeuAlaHisLeuGlyGlnHisAsnLeuGlnLysGlyGlyGlyGlyGlyGlyGlyGly 120
Db      310 ATAGTTCACTGGGCGAGACCAACCTCCAGAAAGAGAGAGGCTGTGAGCAGACCCGAGCA 369
QY      121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
Db      370 GCCACGTAGTCTTCCCGACCCCGGCTTCAACAAAGAGCTCCCGCAACAAAGCAGCCGC 429
QY      141 AsnAspLLeuMetLeuValLysMetAlaSerProValSerLLeuThrTrpAlaValArgPro 160
Db      430 AATGACATCATGCTGTGTGAAGATGAGCATGCCAGTCTCATCATCACTGGGCTGTGAGACCC 489

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QY      161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuLLeuSerGlyTrpGly 180
Db      490 CTCACCCCTCTCTCAAGCTGTGTCACTGTGACACCAAGCTGCTATTTCCGGCTGGGC 549
QY      181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnLLeuThrLle 200
Db      550 AGCAGCTCCAGCCCCCAGTACGCTGCTCAGCTTGCAGTGGCCCAACATCACCAATC 609
QY      201 ILeuGlnHisGlyLysCysGluAsnAlaTyrProGlyAsnLLeuThrAspThrMetValCys 220
Db      610 ATTGAGACCAAGAGTGTGAGAACCGCTTACCCCGCAGATGCACAGACACCATGTGTGT 669
QY      221 AlaSerValGlnGlyGlyLysAspSerCysGlnGlyAspSerGlyLysProLeuVal 240
Db      670 GCCAGGTGCAGAGAGGGGGGCAAGAGCTCTGCGAGGGTGAATCCGGGGGCGCTCGTC 729
QY      241 CysAsnGlnSerLeuGlnGlyLLeuSerTrpGlyGlnAspProCysAlaLLeuThrArg 260
Db      730 TGTAACTAGTCTTCAAGGCAATTATCTCTGGGGCCAGAGATCCGTTGCGATCACCCGA 789
QY      261 LysProGlyValTyrThrLysValCysLysTyrValAspTrpLLeuGlnThrMetLys 280
Db      790 AAGCCTGGTGTCTACAGGAAAGTCTGCAGAAATGTGAGTGGATCCAGAGAGATGAAG 849
QY      281 AsnAsn 282
Db      850 AACAA 855
RESULT 12
LOCUS   BD091587      1301 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION
Novel serine protease BSSP6.
ACCESSION
BD091587
VERSION
BD091587.1 GI:22637198
KEYWORDS
WO 0031257-A/1.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 1301)
AUTHORS
Uemura,H., Okui,A., Komimami,K., Yamaguchi,N. and Mitsui,S.
Novel serine protease BSSP6
Patent: WO 0031257-A 1 02-JUN-2000;
FUSO PHARMACEUTICAL INDUSTRIES LTD, HIDEOTOSHI UEMURA, AKIRA OKUI,
KATSUYA KOMINAMI, NOZOMI YAMAGUCHI, SHINICHI MITSUI
COMMENT
OS Homo sapiens (human)
PN WO 0031257-A/1
PD 02-JUN-2000
PF 19-NOV-1999 WO 1999JP006476
PR 20-NOV-1998 JP 98P 347802
PI HIDEOTOSHI UEMURA, AKIRA OKUI, KATSUYA KOMINAMI, NOZOMI YAMAGUCHI,
SHINICHI MITSUI
PC C12N15/12, C12N9/64, C12N5/06, C12N1/21, C07K16/40, C12P21/08, PC
A01K67/027,
CC G01N33/543
FH Key Location/Qualifiers.
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/mol_type="genomic DNA"
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BASE COUNT      332 a      387 c      330 g      252 t
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Alignment Scores:
Pred. No.:      7,23e-113      Length:      1301
Score:      1523.00      Matches:      282
Percent Similarity:      100.00%      Conservative:      0
Best Local Similarity:      100.00%      Mismatches:      0
Query Match:      100.00%      Indels:      0
DB:      Gaps:      0

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US-09-856-320A-2 (1-282) x BD091587 (1-1301)

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QY      21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleLeu 40
Db      173 AAGGAACCTGGGGCGGCTCTCCCGCCCTCCAGGCCATAGATTCTTGAGTTAAATCCG 232
QY      41 LeuAlaLeuAlaThrGlyLeuValGlyGlyGluThrArgIleIleLysGlyPheGluCys 60
Db      233 CTTCCTCTGGCAACAGGCTTGTAGGGAGAGACAGATCATCAGAGGCTTCAGATGC 292
QY      61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGluLysThrArgLeuLeuGlyCys 80
Db      293 AAGCTCATCTCCAGCCCTGGCAGGAGCCCTGTTGAGAGAGCGGCTACTCTGTGG 352
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Db      353 GCGAGCCTCATCGCCCCAGATGGCTCTGACAGCAGCCACTGCTCAAGCCCGCTAC 412
QY      101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGluGluGlyCysGluGlnThrArgThr 120
Db      413 ATAGTTCACTGGGAGCACAACCTCCAGAGAGAGAGGCTGTGAGCAGACCGGACA 472
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QY      141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
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Db      593 CTCACCTCTCTCTCAGCTGTGTCTCACTGTGGACACAGCTGCTATTCCGGCTGGGGC 652
QY      181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
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Db      713 ATTTAGACACAGAAAGTGAGAACCGCTACCCCGGCAACATCACAGACCCATGTGTGT 772
QY      221 AlaSerValGlnGluGlyLysAspSerCysGlnGlyAspSerGlyValProLeuVal 240
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QY      241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
Db      833 TGTAAACCACTCTTCAAGGATTAATCTCTGGGGCAGAGATCCGTTGTCATCACCGCA 892
QY      261 LysProGlyValIleThrLysValCysLysTyrValAspTrpIleGlnIleThrMetLys 280
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QY      281 AsnAsn 282
Db      953 AACCAAT 958

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RESULT 13

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 LOCUS Homo sapiens mRNA for prostate-type hippostasin, complete cds.
 DEFINITION
 AB041036
 AB041036.1 GI:8574438
 VERSION
 KEYWORDS prostate-type hippostasin.
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (sites)
 AUTHORS Mitsui, S., Yamada, T., Okui, A., Komiyama, K., Uemura, H. and Yamaguchi, N.
 TITLE A novel isoform of a kallikrein-like protease, TUSP/hippostasin, (PRSS20), is expressed in the human brain and prostate
 JOURNAL Biochem. Biophys. Res. Commun. 272 (1), 205-211 (2000)
 MEDLINE 20329229
 PUBMED 10872828
 REFERENCE 2 (bases 1 to 1301)
 AUTHORS Yamaguchi, N. and Mitsui, S.
 TITLE Direct Submission
 JOURNAL Submitted (31-MAR-2000) Nozomi Yamaguchi, Kyoto Prefectural University of Medicine, Res. Ins. Geriatrics; Kawarachi Hirokoji, Kyoto, Kyoto 602-8566, Japan (E-mail: nozomi@koto.kpu-m.ac.jp, Tel:81-75-251-5848, Fax:81-75-251-5848)
 FEATURES
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 CDS
 332 a 387 c 330 g 252 c

BASE COUNT 332 a 387 c 330 g 252 c
 ORIGIN
 Alignment Scores:
 Pred. No.: 7,23e-113 Length: 1301
 Score: 1523.00 Matches: 282
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-856-320A-2 (1-282) x AB041036 (1-1301)

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Db      173 AAGGAACCTGGGGCGGCTCTCCCGCCCTCCAGGCCATAGATTCTTGAGTTAAATCCG 232
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Db      233 CTTCCTCTGGCAACAGGCTTGTAGGGAGAGACAGATCATCAGAGGCTTCAGATGC 292
QY      61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGluLysThrArgLeuLeuGlyCys 80
Db      293 AAGCTCATCTCCAGCCCTGGCAGGAGCCCTGTTGAGAGAGCGGCTACTCTGTGG 352
QY      81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
Db      353 GCGAGCCTCATCGCCCCAGATGGCTCTGACAGCAGCCACTGCTCAAGCCCGCTAC 412
QY      101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGluGluGlyCysGluGlnThrArgThr 120
Db      413 ATAGTTCACTGGGAGCACAACCTCCAGAGAGAGGCTGTGAGCAGACCGGACA 472
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QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
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 QY 261 LysProGlyValTyThrLysValCysLysTyValAspTrpIleGlnGlnThrMetLys 280
 DB 893 AAGCGCTGTCTACACGAAAGCTGCAATATGTGACTGATCCAGAGAGCATGAAG 952
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 DB 953 AACAAAT 958

RESULT 14

AR098430

LOCUS AR098430 1314 bp DNA linear PAT 14-FEB-2001
 DEFINITION Sequence 2 from patent US 6075136.
 ACCESSION AR098430
 VERSION AR098430.1 GI:12807687

KEYWORDS

SOURCE Unknown.

ORGANISM

Unclassified.

REFERENCE 1 to 1314

AUTHORS Tang, Y. Tom, Corley, N.C. and Guegler, K.J.

TITLE Prostate-associated serine protease

JOURNAL Patent: US 6075136-A 2 13-JUN-2000;

FEATURES Location/Qualifiers

1..1314

/organism="unknown"

BASE COUNT 320 a 400 c 337 g 257 t

ORIGIN

Alignment Scores:

Pred. No.: 7,31e-113 Length: 1314

Score: 1523.00 Matches: 282

Best Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-09-856-320A-2 (1-282) x AR098430 (1-1314)

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 DB 188 AAGGAACCTGGGGCCCGCTCTCCCTCCAGGCAATGAGATTCTGAGTTAATCTCG 247
 QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyGlnThrArgIleIleLysGlyPheGlyCys 60
 DB 248 CTTGCTCTGGCAACAGGCTTGTAGGGGAGAGACAGATCATCAAGGGTTCCAGTCC 307

QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGluLysThrArgLeuLeuCysGly 80
 DB 308 AAGCTCTACTCCACACCCCTGGCAGGACAGCCCTGTTGAGAAACCCGGCTACTCTGGG 367
 QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTy 100
 DB 368 GCGAGCTCATGAGCCCGGAGATGAGTCTCTGACAGAGCCCACTGCTCAAGCCCGCTAC 427
 QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlnGlnGlyCysGlnGlnThrArgThr 120
 DB 428 ATAGTTCACTGGGGCAGACAACTCCAGAAAGGAGAGGCTGTGAGACAGACCCGAGCA 487
 QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
 DB 488 GCCACTGACTCTTCTCCCAACCCCGGCTTCAACAAACAGCTTCCCAACAAAGACACCCG 547
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 DB 548 AATGACATCATGCTGTGAAGATGATGCATGCGCATGCTCATCCTGGGCTGGGACCC 607
 QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
 DB 608 CTCACCTCTCTCTCCAGCTGTGTGCTGCTGCGCAGCAGCTGCTCATTTCCCGCTGGG 667
 QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
 DB 668 AGCAGCTCCAGCCCCAGTTAGCTGCTGCTCCACACCTTGCGATGCCCAACATCACCATC 727
 QY 201 IleGluHisGlnLysCysGluAsnAlaTyProGlyAsnIleThrAspThrMetValCys 220
 DB 728 ATTGACACACAGAAAGTGTGAAGAGCGCTACCCCGGCAACATCAGACACATGCTGT 787
 QY 221 AlaSerValGlnGlnGlyGlyLysAspSerCysGlnGlyAspSerGlyGlyProLeuVal 240
 DB 788 GCCAGCTCAGAGAGAGGGGCAAGAGACTCTGCGCAGGGTGACTCCGGGGCCCTCTGCTC 847
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 DB 848 TGTAACTAGTCTCTTAAGGCAATTAATCTCTGGGGCCAGGATCCTGTGCGATCACCAG 907
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 DB 908 AAGCGCTGTCTACACGAAAGCTGCAATATGTGACTGATCCAGAGAGCATGAAG 967
 QY 281 AsnAsn 282
 DB 968 AACAAAT 973

RESULT 15

BD130920

LOCUS BD130920 1314 bp DNA linear PAT 18-SEP-2002
 DEFINITION Serine protease relating to human prostate.
 ACCESSION BD130920
 VERSION BD130920.1 GI:23225865

KEYWORDS

JOURNAL

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 1314)

AUTHORS Tang, T.Y., Corley, N.C. and Guegler, K.J.

TITLE Serine protease relating to human prostate

JOURNAL Patent: JP 2002503471-A 1 05-FEB-2002;

COMMENT INCYTE PHARMACEUTICALS INC

OS Homo sapiens (human)

PN JP 2002503471-A/1

PD 05-FEB-2002

PF 05-FEB-1999 JP 2000531566

PI 17-FEB-1998 US 09/025059

PC C12N15/09, A61K38/48, A61K45/00, A61P13/08, A61P15/00, A61P35/00, C07K16/40,

PC C12N1/19, C12N1/21, C12N5/10, C12N9/64, C12Q1/68, C12N15/00, A61K37/
 PC 547, C12N5/00 Location/Qualifiers
 CC 2723646
 FH Key 1.1314
 FT source /organism='Homo sapiens' (human)'
 FT Location/Qualifiers
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 /organism='Homo sapiens'
 /mol_type='genomic DNA'
 /db_xref='taxon:9606'

BASE COUNT 320 a 400 c 337 g 257 t
 ORIGIN

Alignment Scores:
 Pred. No.: 7.31e-113 Length: 1314
 Score: 1523.00 Matches: 282
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-856-320A-2 (1-282) x BD130920 (1-1314)

QY 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAla 20
 DB 128 ATGCAGAGGTTAGAGGCTGGCGGACTGGAAGTCATCCGGCAGAGGTTCCACAGAGCC 187
 QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeu 40
 DB 188 AAGGAACCTGGGGCCCGCTCTCCCTCCCGCCATGAGCATGCGATTCTGCAATCCTG 247
 QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyIleThrArgIleIleLysGlyPheGlyCys 60
 DB 248 CTTCCTCTGGCAACAGGCTGTAGGGGAGAGACCAAGATCATCAAGGGTTCCAGATCC 307
 QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGluLysThrArgLeuLeuCysGly 80
 DB 308 AAGCTCACTCCAGCCCTGGCAGGAGCCCTGTTGAGAAAGCGGGCTACTCTGTGG 367
 QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
 DB 368 GCGAGCTCATGCCCCCGAGTGGCTCTCGACAGACGCCCACTGCTCAAGCCCCGCTAC 427
 QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlyCysGluGlnThrArgThr 120
 DB 428 ATAGTTCACTGGGCGAGCAACCTCCGAGAGAGAGGCTGTGAGCAGACCCGAGACA 487
 QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
 DB 488 GCCACTGAATCTTCCCGCCAGCCCGCTTCACAAACAGCTCCCAACAAAGACCAACCGC 547
 QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
 DB 548 AATGACATCATCTCTGTGAAGATGGCATGGCAGTCTCATCATCACTGGGCTGTGCAACC 607
 QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
 DB 608 CTCACCTCTCTCAAGCTGTGTCACTGTGGCACCAAGCTGCTCATTTCCGGCTGGGGC 667
 QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
 DB 668 AGCAGCTCCAGCCCCCAGATTACGCTGTGCTCACACCTTGGCATGGCCCAACATCACATC 727
 QY 201 IleGluHisGlnLysCysGluAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220
 DB 728 ATTGAGACCAAGAGTGTGAAGACCGCTTACCCCGGCAACATCACAGACCACTGGTGTGT 787
 QY 221 AlaSerValGlnGlyGlyLysAspSerCysGlnGlyAspSerGlyIleProLeuVal 240
 DB 788 GCCACGCTGCAGAGAGGGGCAAGGACTCTGCAAGGATGACTCCGGGGGCCCTCTGGTTC 847
 QY 241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260

DB 848 TGTAAACGCTCTTCAAGGCATTATCTCTGGGGCCAGGATCCGTGGCATCACCCGA 907
 QY 261 LysProGlyValTyrThrLysValCysLysTyrValAspTrpIleGlnGluThrMetLys 280
 DB 908 AAGCTGTGTCTACAGCAAGTCTGCAAAATATGTGACTGATCCAGGACCATGAAAG 967
 QY 281 AsnAsn 282
 DB 968 AACCAAT 973

Search completed: October 23, 2003, 18:05:15
 Job time : 4216.2 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2003, 15:46:12 : Search time 41.9413 Seconds
(without alignments)
1067.227 Million cell updates/sec

Title: US-09-856-320a-2

Perfect score: 1523
Sequence: 1 MQRRLRLRLRMKSSGRGLTAA.....GVYTKVCKYVDVIQETMKNN 282

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1523	100.0	282	20	AAV42439
2	1523	100.0	282	21	AAAB11712
3	1523	100.0	282	21	AAAY43636
4	1517	99.6	281	20	AAAY42440
5	1355	89.0	250	21	AAAB21325
6	1355	89.0	250	21	AAAY9390
7	1355	89.0	250	22	AAAB50479
8	1355	89.0	250	22	AAU12424
9	1355	89.0	250	22	AAAB61139

10	1355	89.0	250	23	ABG61816
11	1355	89.0	250	23	ABB95526
12	1355	89.0	250	23	ABB84920
13	1355	89.0	250	23	AAU83684
14	1355	89.0	250	24	AAU66822
15	1355	89.0	250	24	ABU67098
16	1355	89.0	250	24	ABU59903
17	1355	89.0	250	24	ABU56739
18	1332.5	87.5	275	21	AAAB1714
19	1332.5	87.0	250	20	AAV36093
20	1324	86.9	248	22	AAE08017
21	1279.5	84.0	247	23	ABG70276
22	1252	82.2	228	21	AAAB21312
23	1237	80.6	289	21	AAAB36483
24	1237	80.6	289	22	AAAB67543
25	1187	77.9	276	21	AAAB1713
26	758	49.8	251	22	AAU16971
27	756	49.6	250	21	AAAB21298
28	756	49.6	250	23	ABP64969
29	754	49.5	247	22	AAU23217
30	748	49.1	246	20	AAW89041
31	748	49.1	246	22	ABB51196
32	742.5	48.8	296	21	AAAB21297
33	736	48.3	247	22	AAU86677
34	736	48.3	247	22	AAU23752
35	736	48.3	247	22	AAU17043
36	698.5	45.9	260	17	AAW10694
37	698.5	45.9	260	18	AAW12393
38	698.5	45.9	260	23	ABB57219
39	697	45.8	275	21	AAAB21311
40	696	45.7	320	23	AAE19166
41	696	45.7	320	23	AAU83732
42	692.5	45.5	256	23	AAU79390
43	690	45.3	260	20	AAV41744
44	690	45.3	260	20	AAV32852
45	690	45.3	260	20	AAV03220

ALIGNMENTS

RESULT 1	AAV42439	strand: Protein; 282 AA.
ID	AAV42439	
AC	AAV42439;	
XX		
DT	08-DEC-1999	(first entry)
XX		
DE	CASB12 amino acid sequence.	
XX		
KW	neuropilin; cancer; assay; inhibitor; serine protease; immunogenic;	
KW	autoimmune disease.	
OS	Homo sapiens.	
XX		
PN	WO9949055-A1.	
XX		
PD	30-SEP-1999.	
XX		
PF	17-MAR-1999;	99WO-EP01894.
XX		
PR	20-MAR-1998;	98GB-0006095.
XX		
PA	(SMK) SMITHKLINE BEECHAM BIOLOGICALS.	
XX		
PI	Bruck CEM, Cassart J, Coche T, Vinals-bassols C;	
DR	WPI; 1999-580450/49.	
XX		
DR	N-PSDB; AA22638.	
XX		
PT	New human serine protease CASB12, for treatment, prevention and	
PT	diagnosis of cancer and autoimmune diseases	

Prostate cancer-as
Human angiogenesis
Human PRO1279 prot
Human PRO protein,
Human PRO polypept
Human secreted/Lira
Novel secreted and
Lung cancer-associ
Human serine prote
Extended human sec
Human PS133 consen
Human Serine Prote
Human TISP. Homo
Fusion gene with h
Amino acid sequenc
Mouse serine prote
Human novel secret
Human KLR-L3 prote
Human protein SEQ
Human novel enzyme
Polypeptide fragme
Human secreted pro
Human KLR-L3 prote
Novel human connec
Novel human enzyme
Human novel secret
Human recombinant
Mouse neuropilin pr
Mouse ischaemic co
Human neuropilin.
Human protease, PR
Amino acid sequenc
Novel human kallik
Human PRO122 prote
Human serine prote
Amino acid sequenc

XX Claim 3, Page 48, 58pp; English.

PS This is the amino acid sequence of the CASB12 protein. The nucleotide
 XX sequence of AA222638 shows homology with neuropilin and the encoded
 CC protein AA42439 is structurally related to other proteins of the
 CC serine protease family, having homology and/or structural similarity
 CC with neuropilin. It is expected that as well as similar structure, these
 CC proteins will also share similar biological functions and properties.
 CC The CASB12 polypeptides and polynucleotides can be used to develop
 CC methods for identifying agonists and antagonists/inhibitors of these
 CC molecules, and thereby treating conditions associated with CASB12
 CC polypeptide imbalance. The invention also provides for diagnostic assays
 CC for detecting diseases associated with inappropriate CASB12 polypeptide
 CC activity or levels.
 CC Since CASB12 is either specifically expressed or highly over-expressed
 CC in tumors compared to normal cells, the polypeptides and polynucleotides
 CC of the invention are believed to be important immunogens for specific
 CC prophylactic or therapeutic immunization against tumors. The
 CC polypeptides and polynucleotides can therefore be targeted by antigen
 CC specific immune reactions (which result in the destruction of the tumor
 CC cell) or they can be used to diagnose the occurrence of tumor cells

XX Sequence 282 AA:

Query Match 100.0%; Score 1523; DB 20; Length 282;
 Best Local Similarity 100.0%; Pred. No. 1.5e-134;
 Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORLWRLRWKSSGGLTAKEPGARSSPLQAMRILOLLALATGVLGGERRIIKGPEC 60
 Db 1 MORLWRLRWKSSGGLTAKEPGARSSPLQAMRILOLLALATGVLGGERRIIKGPEC 60
 QY 61 KHSQPMQALFEKRLTLCGATLLAPRWLLTAHCLKPRYIVHLCQHNLOKEEGCEQRT 120
 Db 61 KHSQPMQALFEKRLTLCGATLLAPRWLLTAHCLKPRYIVHLCQHNLOKEEGCEQRT 120
 QY 121 ATESEFPHPGPNNSLPKNDHRNDIMLVKMASPVSIWAVRPLTLSSRCVTAGTSCGISG 180
 Db 121 ATESEFPHPGPNNSLPKNDHRNDIMLVKMASPVSIWAVRPLTLSSRCVTAGTSCGISG 180
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 Db 181 STSSPOLRPLPHTLRCAANTIIHOKCENAYPGNITDTWVCASVQEGKDCGSDGGPLV 240
 QY 241 CNOISLGIISWGQDPCATIRKPGVYTKVCKYVDWIOETMKN 282
 Db 241 CNOISLGIISWGQDPCATIRKPGVYTKVCKYVDWIOETMKN 282

RESULT 2
 AAB11712
 ID AAB11712 standard; Protein, 282 AA.

XX AAB11712;

XX 23-OCT-2000 (first entry)

XX Human serine protease BSSP6 (hbssP6) SEQ ID NO:2.

XX BSSP6; serine protease; human; hbssP6; mouse; mbssP6; brain;
 KW diagnostic marker; antibody; transgenic animal; Alzheimer's disease;
 KW epilepsy; cancer; inflammation; infertility; pancreatitis;
 KW prostatic hypertrophy.

XX Homo sapiens.

XX WO200031257-A1.

XX 02-JUN-2000.

XX 19-NOV-1999; 99WO-0P06476.

PR 20-NOV-1998; 98JP-0347802.

XX (FUSO) FUSO PHARM IND LTD.

XX Uemura H, Okui A, Kominami K, Yamaguchi N, Mitsui S;

XX WPI/2000-400067/34.

XX N-PSDB: AAA61763.

PT Serine protease BSSP6, useful in detecting homologs, mutants and
 PT polymorphic variants as markers for diagnosis of Alzheimer's disease,
 PT epilepsy, cancer, inflammation, infertility and prostate hypertrophy,
 PT using blood or other tissues

XX Claim 1; Page 69-70; 94pp; Japanese.

CC The invention relates to novel serine proteases designated BSSP6
 CC (AAB11712-B11714), and to nucleic acids encoding them (AAA61763-A61765).
 CC The invention also relates to vectors and transformants comprising BSSP6
 CC nucleic acids; transgenic animals in which the expression level of BSSP6
 CC can be varied; and an mbssP6 knockout mouse. The invention additionally
 CC encompasses anti-BSSP6 antibodies and methods of production of such
 CC antibodies, methods of BSSP6 detection using the antibodies, and the
 CC use of BSSP6 proteins or fragments as diagnostic markers for certain
 CC medical conditions. Nucleotides encoding BSSP6 were initially
 CC isolated in a human brain cDNA library using degenerate PCR primers
 CC (AA61795-A61796) based on conserved regions of serine proteases. The
 CC BSSP6 serine proteases and nucleotides encoding them are useful in
 CC detecting homologs, mutants and polymorphic variants in biological
 CC samples (e.g., blood, urine, brain, prostate gland, placenta, testis
 CC and spleen) as diagnostic markers for conditions such as Alzheimer's
 CC disease, epilepsy, cancer, inflammation, infertility and prostatic
 CC hypertrophy. Sequences AAB11712 and AAB11714 represent human BSSP6
 CC variants (hbssP6), and sequence AAB11713 represents murine BSSP6
 CC (mbssP6).

XX Sequence 282 AA:

Query Match 100.0%; Score 1523; DB 21; Length 282;
 Best Local Similarity 100.0%; Pred. No. 1.5e-134;
 Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORLWRLDWKSSGGLTAKEPGARSSPLQAMRILOLLALATGVLGGERRIIKGPEC 60
 Db 1 MORLWRLDWKSSGGLTAKEPGARSSPLQAMRILOLLALATGVLGGERRIIKGPEC 60
 QY 61 KHSQPMQALFEKRLTLCGATLLAPRWLLTAHCLKPRYIVHLCQHNLOKEEGCEQRT 120
 Db 61 KHSQPMQALFEKRLTLCGATLLAPRWLLTAHCLKPRYIVHLCQHNLOKEEGCEQRT 120
 QY 121 ATESEFPHPGPNNSLPKNDHRNDIMLVKMASPVSIWAVRPLTLSSRCVTAGTSCGISG 180
 Db 121 ATESEFPHPGPNNSLPKNDHRNDIMLVKMASPVSIWAVRPLTLSSRCVTAGTSCGISG 180
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 Db 181 STSSPOLRPLPHTLRCAANTIIHOKCENAYPGNITDTWVCASVQEGKDCGSDGGPLV 240
 QY 241 CNOISLGIISWGQDPCATIRKPGVYTKVCKYVDWIOETMKN 282
 Db 241 CNOISLGIISWGQDPCATIRKPGVYTKVCKYVDWIOETMKN 282

RESULT 3

XX AA43636 standard; Protein, 282 AA.

XX AA43636;

XX 11-FEB-2000 (first entry)

XX A human prostate-associated serum protease (PRASP).

KW Human; prostate-associated serum protease; PRASP; neuropsin; PSA;
 KW Incyte clone 2723646; reproductive disorder; cancer;
 KW abnormal prolactin production; infertility; tubal disease;
 KW ovulatory defect; endometriosis; polycystic ovary syndrome;
 KW autoimmune disorder; ectopic pregnancy; breast cancer;
 KW abnormal spermatogenesis; testicular cancer; adenocarcinoma; leukaemia;
 KW lymphoma; melanoma; myeloma; sarcoma; teratocarcinoma.
 XX Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..50 /note= "signal sequence"
 FT Modified-site 13 /note= "potential protein kinase C phosphorylation site"
 FT Disulfide-bond 60 /note= "this corresponding residue in PSA is involved in intramolecular disulphide bond formation"
 FT Disulfide-bond 79 /note= "this corresponding residue in PSA is involved in intramolecular disulphide bond formation"
 FT Active-site 90..95 /note= "serine protease trypsin family active site motif"
 FT Misc-difference 94 /note= "this forms the active site catalytic triad with Asp142 and Ser235"
 FT Disulfide-bond 95 /note= "this corresponding residue in PSA is involved in intramolecular disulphide bond formation"
 FT Modified-site 120 /note= "potential casein kinase II phosphorylation site"
 FT Modified-site 131 /note= "potential N-glycosylation site"
 FT Misc-difference 142 /note= "this forms the active site catalytic triad with His94 and Ser235"
 FT Modified-site 164 /note= "potential protein kinase C phosphorylation site"
 FT Disulfide-bond 174 /note= "this corresponding residue in PSA is involved in intramolecular disulphide bond formation"
 FT Modified-site 192 /note= "potential protein kinase C phosphorylation site"
 FT Disulfide-bond 195 /note= "this corresponding residue in PSA is involved in intramolecular disulphide bond formation"
 FT Modified-site 197 /note= "potential N-glycosylation site"
 FT Modified-site 199 /note= "potential casein kinase II phosphorylation site"
 FT Disulfide-bond 206 /note= "this corresponding residue in PSA is involved in intramolecular disulphide bond formation"
 FT Modified-site 213 /note= "potential N-glycosylation site"
 FT Disulfide-bond 220 /note= "this corresponding residue in PSA is involved in intramolecular disulphide bond formation"
 FT Modified-site 222 /note= "potential casein kinase II phosphorylation site"
 FT Active-site 229..240 /note= "serine protease trypsin family active site motif"
 FT Misc-difference 229 /note= "the corresponding residue (together with Ser235, Gly252 and Gly263) in neuropsin forms a oxyanion hole"

FT Disulfide-bond 231 /note= "this corresponding residue in PSA is involved in intramolecular disulphide bond formation"
 FT Misc-difference 235 /note= "the corresponding residue (together with Asp229, Gly252 and Gly263) in neuropsin forms a oxyanion hole"
 FT Misc-difference 235 /note= "this forms the active site catalytic triad with His94 and Asp142"
 FT Disulfide-bond 241 /note= "this corresponding residue in PSA is involved in intramolecular disulphide bond formation"
 FT Modified-site 242 /note= "potential N-glycosylation site"
 FT Misc-difference 252 /note= "the corresponding residue (together with Asp229, Ser235 and Gly263) in neuropsin forms a oxyanion hole"
 FT Disulfide-bond 256 /note= "this corresponding residue in PSA is involved in intramolecular disulphide bond formation"
 FT Modified-site 259 /note= "potential protein kinase C phosphorylation site"
 FT Misc-difference 263 /note= "the corresponding residue (together with Asp229, Ser235 and Gly252) in neuropsin forms a oxyanion hole"
 FT Modified-site 278 /note= "potential protein kinase C phosphorylation site"
 XX
 XX WO9941387-A2.
 XX 19-AUG-1999.
 PD
 XX 05-FEB-1999; 99WO-US02571.
 XX
 PR 17-FEB-1998; 98US-0025059.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Tang YT, Corley NC, Guegler KJ;
 XX WPI; 2000-012993/01.
 DR N-PSDB; AA230222.
 XX
 PT New prostate-associated serum protease and polynucleotides which identify and encode PRASP, useful for treating reproductive disorders and cancer
 PT
 PS
 XX
 PS Claim 1; Fig 1A-D; 67pp; English.
 CC The present sequence represents human prostate-associated serum protease (PRASP). The protein shows homology to neuropsin, a brain-specific protease in mice, and PSA, a prostate-specific protease in humans. Nucleic acids encoding PRASP were first identified in incyte clone 2723646 from the lung tumour cDNA library. Pharmaceutical compositions containing PRASP, or antibodies to PRASP, and mimetics, agonists, antagonists or inhibitors of PRASP, are used for treating or preventing a reproductive disorder or cancer. Examples of reproductive disorder include, abnormal prolactin production, infertility, tubal disease, ovulatory defects, endometriosis, polycystic ovary syndrome, autoimmune disorders, ectopic pregnancy, breast cancer, abnormal spermatogenesis and testicular cancer. Examples of cancers which may be treated or prevented include adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid and uterus. A vector capable of expressing PRASP or an agonist which modulates the activity of PRASP may be administered to treat or prevent a reproductive disorder or

CC cancer.
 XX Sequence 282 AA;
 SQ Query Match 100.0%; Score 1523; DB 21; Length 282;
 Best Local Similarity 100.0%; Pred. No. 1.5e-134;
 Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORLRMLRWKSSGRLTAKEPGARSSPLQAMRIQLILALATGLVGETRIIKGFEC 60
 DB 1 MORLRMLRWKSSGRLTAKEPGARSSPLQAMRIQLILALATGLVGETRIIKGFEC 60
 QY 61 KPHSOPWQALFEKTRILCGATLAPRWLLTAHCLKPRYIVHLGQHNLOKEEGCEQRT 120
 DB 61 KPHSOPWQALFEKTRILCGATLAPRWLLTAHCLKPRYIVHLGQHNLOKEEGCEQRT 120
 QY 121 ATESEFPHPGFNNSLPNKDHNDIMLVKMASPVSIITWAVRPLTSSRCVTAGTSCGISG 180
 DB 121 ATESEFPHPGFNNSLPNKDHNDIMLVKMASPVSIITWAVRPLTSSRCVTAGTSCGISG 180
 QY 181 STSSPOLRLPHTLRKANITIIIEHOKCENAYPGNITDTWVCASVQEGKDCQDGSGL 240
 DB 181 STSSPOLRLPHTLRKANITIIIEHOKCENAYPGNITDTWVCASVQEGKDCQDGSGL 240
 QY 241 CNOSLOGIISWGODPCATTRKPGVYTKVCKYVDMIOETMKN 282
 DB 241 CNOSLOGIISWGODPCATTRKPGVYTKVCKYVDMIOETMKN 282

RESULT 4
 AAY42440
 ID AAY42440 standard; Protein; 281 AA.
 AC AAY42440;
 XX 08-DEC-1999 (first entry)
 DT CASB12 polypeptide derived from Expressed Sequence Tag products.
 XX CASB12 polypeptide derived from Expressed Sequence Tag products.
 DE CASB12 polypeptide derived from Expressed Sequence Tag products.
 XX CASB12 polypeptide derived from Expressed Sequence Tag products.
 KW neurospisin; cancer; assay; inhibitor; serine protease; immunogenic;
 XX autoimmune disease.
 OS Homo sapiens.
 XX Homo sapiens.
 OS Homo sapiens.
 XX Homo sapiens.
 PN WO9949055-A1.
 XX WO9949055-A1.
 PD 30-SEP-1999.
 XX 30-SEP-1999.
 PF 17-MAR-1999; 99WO-EP01894.
 XX 17-MAR-1999; 99WO-EP01894.
 PR 20-MAR-1998; 98GB-0006095.
 XX 20-MAR-1998; 98GB-0006095.
 PA (SMK) SMITHKLINE BEECHAM BIOLOGICALS.
 XX (SMK) SMITHKLINE BEECHAM BIOLOGICALS.
 PI Bruck CEM, Cassart J, Coche T, Vinals-bassols C;
 XX Bruck CEM, Cassart J, Coche T, Vinals-bassols C;
 DR WPI; 1999-580450/49.
 XX WPI; 1999-580450/49.
 DR N-PSDB; AA222639.
 XX N-PSDB; AA222639.
 PT New human serine protease CASB12, for treatment, prevention and
 XX diagnosis of cancer and autoimmune diseases -
 PS Claim 27; Page 49-50; 58pp; English.
 CC This is the amino acid sequence of CASB12 protein, derived from an
 CC Expressed Sequence Tag (EST) search for tumor-specific and
 CC tumor-associated antigens. The nucleotide sequence of AA222638 shows
 CC homology with neurospisin and the encoded protein AAY42439 is structurally
 CC related to other proteins of the serine protease family, having homology
 CC and/or structural similarity with neurospisin. It is expected that as well
 CC as similar structure, these proteins will also share similar biological
 CC functions and properties.
 CC The CASB12 polypeptides and polynucleotides can be used to develop

CC methods for identifying agonists and antagonists/inhibitors of these
 CC molecules, and thereby creating conditions associated with CASB12
 CC polypeptide imbalance. The invention also provides for diagnostic assays
 CC for detecting diseases associated with inappropriate CASB12 polypeptide
 CC activity or levels.
 CC Since CASB12 is either specifically expressed or highly over-expressed
 CC in tumors compared to normal cells, the polypeptides and polynucleotides
 CC of the invention are believed to be important immunogens for specific
 CC prophylactic or therapeutic immunization against tumors. The
 CC polypeptides and polynucleotides can therefore be targeted by antigen
 CC specific immune reactions (which result in the destruction of the tumor
 CC cell) or they can be used to diagnose the occurrence of tumor cells

QY 1 MORLRMLRWKSSGRLTAKEPGARSSPLQAMRIQLILALATGLVGETRIIKGFEC 60
 DB 1 MORLRMLRWKSSGRLTAKEPGARSSPLQAMRIQLILALATGLVGETRIIKGFEC 60
 QY 61 KPHSOPWQALFEKTRILCGATLAPRWLLTAHCLKPRYIVHLGQHNLOKEEGCEQRT 120
 DB 61 KPHSOPWQALFEKTRILCGATLAPRWLLTAHCLKPRYIVHLGQHNLOKEEGCEQRT 120
 QY 121 ATESEFPHPGFNNSLPNKDHNDIMLVKMASPVSIITWAVRPLTSSRCVTAGTSCGISG 180
 DB 121 ATESEFPHPGFNNSLPNKDHNDIMLVKMASPVSIITWAVRPLTSSRCVTAGTSCGISG 180
 QY 181 STSSPOLRLPHTLRKANITIIIEHOKCENAYPGNITDTWVCASVQEGKDCQDGSGL 240
 DB 181 STSSPOLRLPHTLRKANITIIIEHOKCENAYPGNITDTWVCASVQEGKDCQDGSGL 240
 QY 241 CNOSLOGIISWGODPCATTRKPGVYTKVCKYVDMIOETMKN 281
 DB 241 CNOSLOGIISWGODPCATTRKPGVYTKVCKYVDMIOETMKN 281

RESULT 5
 AAB21325
 ID AAB21325 standard; Protein; 250 AA.
 AC AAB21325;
 XX 02-FEB-2001 (first entry)
 DT Human TLSP.
 XX Human TLSP.
 DE Human TLSP.
 XX Human TLSP.
 KW Human; KUK-L1; KUK-L2; KUK-L3; KUK-L4; KUK-L5; KUK-L6; TLSP;
 XX trypsin-like serine protease; kallikrein-like protein; serine protease;
 KW cytosolic; cancer; prostrate cancer.
 OS Homo sapiens.
 XX Homo sapiens.
 PN WO200053776-A2.
 XX WO200053776-A2.
 PD 14-SEP-2000.
 XX 14-SEP-2000.
 PF 09-MAR-2000; 2000WO-CA00258.
 XX 09-MAR-2000; 2000WO-CA00258.
 PR 11-MAR-1999; 99US-0124260.
 XX 11-MAR-1999; 99US-0124260.
 PR 01-APR-1999; 99US-0127386.
 XX 01-APR-1999; 99US-0127386.
 PR 21-JUL-1999; 99US-0144919.
 XX 21-JUL-1999; 99US-0144919.
 PA (MOUNT) MOUNT SINAI HOSPITAL.
 XX (MOUNT) MOUNT SINAI HOSPITAL.
 PI Yousef GM, Diamandis EP;
 XX Yousef GM, Diamandis EP;
 DR WPI; 2000-587440/55.
 XX WPI; 2000-587440/55.
 PT New kallikrein-like (KUK-L) proteins for diagnosing and treating KUK-L

PT protein mediated disorders, especially cancer. -
XX
PS Example 5; Fig 27; 184p; English.
XX
CC The present sequence is human trypsin-like serine protease (TLSP), a
CC member of the serine protease family. Kallikreins and
CC kallikrein-like proteins are a subgroup of the serine protease enzyme
CC family. They catalyze the selective cleavage of specific polypeptide
CC precursors to release peptides with potent biological activity. Nucleic
CC acids encoding kallikrein-like proteins KLK-11, KLK-12, KLK-13, KLK-14,
CC KLK-15 and KLK-16 have been isolated. The proteins are useful in the
CC treatment, monitoring and diagnosis of cancers, especially prostate
CC cancer. They can also be used to identify a substance that can associate
CC with or mediate the biological activity of the proteins. Antibodies can
CC be used to treat conditions mediated by the kallikrein-like proteins.
XX
SQ Sequence 250 AA;
Query Match 89.0%; Score 1355; DB 21; Length 250;
Best Local Similarity 100.0%; Pred. No. 7,6e-119;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 33 MAILLILALATGLVGETRIIKGFECRPHSQPQALFETRLICGATLIAPWLLTA 92
DB 1 MAILLILALATGLVGETRIIKGFECRPHSQPQALFETRLICGATLIAPWLLTA 60
QY 93 AHCLPRYIVHLGOHNLQKEGCEOTRTATESPHGFENNSLPNDHRNDILVMASPV 152
DB 61 AHCLPRYIVHLGOHNLQKEGCEOTRTATESPHGFENNSLPNDHRNDILVMASPV 120
QY 153 SITMAVRPLTSSRCVTAGTSCILISGWSTSSPOLRLPHTLRCANITIIIEHOKENAVPG 212
DB 121 SITMAVRPLTSSRCVTAGTSCILISGWSTSSPOLRLPHTLRCANITIIIEHOKENAVPG 180
QY 213 NITDMVACSVQEGKDSQSGPPLVNOGLGIISGQDPCAITRKPGYITVCKXV 272
DB 181 NITDMVACSVQEGKDSQSGPPLVNOGLGIISGQDPCAITRKPGYITVCKXV 240
QY 273 DWIOETMKNN 282
DB 241 DWIOETMKNN 250
RESULT 6
AA99390
ID AA99390 standard; Protein; 250 AA.
XX
AC AA99390;
XX
DT 08-AUG-2000 (first entry)
XX
DE Human PRO1279 (UNO649) amino acid sequence SEQ ID NO:170.
XX
KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening.
XX
OS Homo sapiens.
XX
FN WO200012708-A2.
XX
PD 09-MAR-2000.
XX
PF 01-SEP-1999; 99WO-US20111.
XX
PR 01-SEP-1998; 98US-0098716.
PR 01-SEP-1998; 98US-0098749.
PR 01-SEP-1998; 98US-0098750.
PR 02-SEP-1998; 98US-0098803.
PR 02-SEP-1998; 98US-0098821.
PR 02-SEP-1998; 98US-0098843.
PR 09-SEP-1998; 98US-0099536.
PR 09-SEP-1998; 98US-0099596.
PR 09-SEP-1998; 98US-0099598.

PR 09-SEP-1998; 98US-0099602.
PR 09-SEP-1998; 98US-0099642.
PR 10-SEP-1998; 98US-0099741.
PR 10-SEP-1998; 98US-0099754.
PR 10-SEP-1998; 98US-0099763.
PR 10-SEP-1998; 98US-0099792.
PR 10-SEP-1998; 98US-0099808.
PR 10-SEP-1998; 98US-0099812.
PR 10-SEP-1998; 98US-0099816.
PR 15-SEP-1998; 98US-0100385.
PR 15-SEP-1998; 98US-0100388.
PR 15-SEP-1998; 98US-0100390.
PR 16-SEP-1998; 98US-0100684.
PR 16-SEP-1998; 98US-0100627.
PR 16-SEP-1998; 98US-0100661.
PR 16-SEP-1998; 98US-0100662.
PR 16-SEP-1998; 98US-0100664.
PR 17-SEP-1998; 98US-0100683.
PR 17-SEP-1998; 98US-0100684.
PR 17-SEP-1998; 98US-0100710.
PR 17-SEP-1998; 98US-0100711.
PR 17-SEP-1998; 98US-0100911.
PR 17-SEP-1998; 98US-0100930.
PR 18-SEP-1998; 98US-0100848.
PR 18-SEP-1998; 98US-0100849.
PR 18-SEP-1998; 98US-0101014.
PR 18-SEP-1998; 98US-0101068.
PR 18-SEP-1998; 98US-0101071.
PR 22-SEP-1998; 98US-0101279.
PR 23-SEP-1998; 98US-0101471.
PR 23-SEP-1998; 98US-0101472.
PR 23-SEP-1998; 98US-0101474.
PR 23-SEP-1998; 98US-0101476.
PR 23-SEP-1998; 98US-0101477.
PR 23-SEP-1998; 98US-0101479.
PR 24-SEP-1998; 98US-0101738.
PR 24-SEP-1998; 98US-0101741.
PR 24-SEP-1998; 98US-0101743.
PR 24-SEP-1998; 98US-0101744.
PR 24-SEP-1998; 98US-0101915.
PR 24-SEP-1998; 98US-0101916.
PR 29-SEP-1998; 98US-0102207.
PR 29-SEP-1998; 98US-0102209.
PR 29-SEP-1998; 98US-0102240.
PR 29-SEP-1998; 98US-0102307.
PR 29-SEP-1998; 98US-0102330.
PR 29-SEP-1998; 98US-0102331.
PR 30-SEP-1998; 98US-0102484.
PR 30-SEP-1998; 98US-0102487.
PR 30-SEP-1998; 98US-0102570.
PR 30-SEP-1998; 98US-0102571.
PR 01-OCT-1998; 98US-0102684.
PR 01-OCT-1998; 98US-0102687.
PR 02-OCT-1998; 98US-0102965.
PR 06-OCT-1998; 98US-0103258.
PR 06-OCT-1998; 98US-0103449.
PR 07-OCT-1998; 98US-0103314.
PR 07-OCT-1998; 98US-0103315.
PR 07-OCT-1998; 98US-0103328.
PR 07-OCT-1998; 98US-0103335.
PR 07-OCT-1998; 98US-0103396.
PR 07-OCT-1998; 98US-0103401.
PR 08-OCT-1998; 98US-0103633.
PR 08-OCT-1998; 98US-0103678.
PR 08-OCT-1998; 98US-0103679.
PR 08-OCT-1998; 98US-0103711.
PR 14-OCT-1998; 98US-0104257.
PR 20-OCT-1998; 98US-0104987.
PR 20-OCT-1998; 98US-0105002.
PR 21-OCT-1998; 98US-0105002.
PR 21-OCT-1998; 98US-0105104.
PR 22-OCT-1998; 98US-0105169.
PR 22-OCT-1998; 98US-0105266.

CC dermatological; immunosuppressive; antiinflammatory; immunostimulant;
 CC anti-HIV; cytostatic; cardiant; anti-angiogenic; ophthalmological;
 CC neuroprotective; nootropic; anticonvulsant; antialzheimer's; vascular;
 CC antiparkinsonian; antimicrobial; and vulnerary. (I) and (II) can be used
 CC in gene therapy and vaccine production. (I) and (II) can be used in the
 CC prevention, diagnosis and treatment of immune disorders (e.g. multiple
 CC sclerosis, systemic lupus erythematosus and human immunodeficiency virus
 CC (HIV) infections), hyperproliferative disorders (e.g. cancers and
 CC Gaucher's disease), cardiovascular diseases (e.g. simillar syndrome,
 CC Chaga's cardiomyopathy and coronary arteriosclerosis), angiogenic
 CC disorders (e.g. corneal graft neovascularisation and diabetic
 CC retinopathy), neurological disorders (e.g. Huntington's chorea,
 CC Alzheimer's disease and Parkinson's disease), infectious diseases and/or
 CC for promoting wound healing, regeneration and/or chemotaxis. ABA3185 to
 CC ABA3193 and ABA50300 represent sequences used in the exemplification of
 CC the present invention.

XX Sequence 250 AA;

Query Match 89.0%; Score 1355; DB 22; Length 250;

Best Local Similarity 100.0%; Pred. No. 7,6e-119; Indels 0; Gaps 0;
 Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 MRILQILALATGLVGETRIIKGFECCKPHSQPQALFEKTRLLCGATLIAPRWLTA 92
 DB 1 MRILQILALATGLVGETRIIKGFECCKPHSQPQALFEKTRLLCGATLIAPRWLTA 60
 QY 93 AHCLKPRYIVHGOHNLQKEGCEQTRTATESFPHPGFNNSLPNKDHNDIMLVKMASPV 152
 DB 61 AHCLKPRYIVHGOHNLQKEGCEQTRTATESFPHPGFNNSLPNKDHNDIMLVKMASPV 120
 QY 153 SITWAVRPLTSSRCVTACTSCLISGWSSTSSPOLRPLPTLPCANTITIEHOKCENAPG 212
 DB 121 SITWAVRPLTSSRCVTACTSCLISGWSSTSSPOLRPLPTLPCANTITIEHOKCENAPG 180
 QY 213 NITDTMVCASVQEGKDSQGDSPGLVNCGLGIIISWGDPICAITRRKPGVYTVCKXV 272
 DB 181 NITDTMVCASVQEGKDSQGDSPGLVNCGLGIIISWGDPICAITRRKPGVYTVCKXV 240

RESULT 8

AAU12424
 ID AAU12424 standard; Protein; 250 AA.

AC AAU12424;

DT 24-OCT-2001 (first entry)

DE Human PRO1279 polypeptide sequence.

XX Human secretory and transmembrane; PRO; mammalian; cancer; lung;

KM breast; prostate; and carcinoma; tumour necrosis factor- α ; TNF- α ;

KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;

XX adipocyte; A-peptide; factor VIIA; gene therapy.

OS Homo sapiens.

XX WO200140466-A2.

XX 07-JUN-2001.

PF 01-DEC-2000; 2000WO-US32678.

XX 01-DEC-1999; 99WO-US28301.

PR 01-DEC-1999; 99WO-US28634.

PR 02-DEC-1999; 99WO-US28551.

PR 02-DEC-1999; 99WO-US28564.

PR 09-DEC-1999; 99US-0170262.

PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 20-DEC-1999; 99WO-US30999.
 PR 30-DEC-1999; 99WO-US31243.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 10-NOV-2000; 2000WO-US30873.

XX (GENENTECH INC.

XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;

PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AU, Sherwood S;

PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

XX WPI, 2001-408281/43.

DR N-PSDB; AAS21496.

PT Isolated, secretory and transmembrane PRO polypeptide used to detect

PT other PRO polypeptides, link bioactive molecules to cells expressing

PT PRO polypeptides, and detect the presence of mammalian tumours e.g.

PT lung, breast, prostate, cervical

PT Claim 12; Fig 506; 813pp; English.

XX AAU12172-AAU12446 represent novel human secretory and transmembrane
 CC PRO polypeptides. The PRO polypeptides are useful to detect other
 CC PRO polypeptides, to link bioactive molecules to cells expressing
 CC PRO polypeptides, to modulate biological activities of cells expressing
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample.
 CC Some of the 275 sequences are also useful to stimulate the release of
 CC tumour necrosis factor- α (TNF- α) from human blood, the
 CC proliferation or differentiation of chondrocytes, the proliferation or
 CC gene expression in pericyte cells, the release of proteoglycans from
 CC cartilage, the proliferation of inner ear utricular supporting cells or
 CC of T-lymphocytes, the release of a cytokine from peripheral blood
 CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
 CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
 CC to factor VIIa. The PRO polypeptides can be used in assays to identify
 CC molecules involved in binding interactions. The polynucleotides encoding
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy.

XX Sequence 250 AA;

Query Match 89.0%; Score 1355; DB 22; Length 250;

Best Local Similarity 100.0%; Pred. No. 7,6e-119; Indels 0; Gaps 0;
 Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 MRILQILALATGLVGETRIIKGFECCKPHSQPQALFEKTRLLCGATLIAPRWLTA 92
 DB 1 MRILQILALATGLVGETRIIKGFECCKPHSQPQALFEKTRLLCGATLIAPRWLTA 60
 QY 93 AHCLKPRYIVHGOHNLQKEGCEQTRTATESFPHPGFNNSLPNKDHNDIMLVKMASPV 152
 DB 61 AHCLKPRYIVHGOHNLQKEGCEQTRTATESFPHPGFNNSLPNKDHNDIMLVKMASPV 120

QY 153 SITMAVRPLTSSRCVTAGTSCGISWGSTSSPOLRLPHTLRCAANTITIEHOKENAYPG 212
 DB 121 SITMAVRPLTSSRCVTAGTSCGISWGSTSSPOLRLPHTLRCAANTITIEHOKENAYPG 180
 QY 213 NITDTMVCASVOEGKDCSCGDSGGLVNCNOSLOGIISWGDDPCAITRKPGVYTKVKYV 272
 DB 181 NITDTMVCASVOEGKDCSCGDSGGLVNCNOSLOGIISWGDDPCAITRKPGVYTKVKYV 240
 QY 273 DWIOETMKNN 282
 DB 241 DWIOETMKNN 250
 RESULT 9
 ID AAB66139 standard; protein; 250 AA.
 AC AAB66139;
 XX
 DT 02-APR-2001 (first entry)
 DE Protein of the invention #51.
 XX
 KW Secreted; transmembrane; gene therapy.
 XX
 OS Unidentified.
 XX
 PN WO200078961-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 18-FEB-2000; 2000WO-US04342.
 XX
 PR 23-JUN-1999; 99US-0141037.
 PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 01-SEP-1999; 99WO-US20111.
 PR 29-OCT-1999; 99US-0162506.
 PR 30-NOV-1999; 99WO-US28313.
 PR 02-DEC-1999; 99WO-US28551.
 PR 16-DEC-1999; 99WO-US30095.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00376.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
 PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
 PI Pan J, Paoletti NF, Roy MA, Smith V, Stewart TA, Tumas D;
 PI Watanabe CK, Williams PM, Wood WI;
 XX
 DR WPI; 2001-071395/08.
 XX
 PT Secreted and transmembrane proteins and nucleic acids designated PRO,
 PT useful as hybridization probes, in chromosome and gene mapping and gene
 PT therapy -
 XX
 PS Claim 1; Fig 102; 787bp; English.
 XX
 CC The present invention relates to secreted and transmembrane proteins.
 CC These proteins and the DNA encoding them may be used as hybridization
 CC probes, in chromosome and gene mapping and in the generation of
 CC anti-sense RNA and DNA. They may also be used to generate either
 CC transgenic animals or knockout animals which are in turn useful for
 CC development and screening of therapeutically useful reagents.
 CC The nucleic acids may also be used in gene therapy.
 XX
 SQ Sequence 250 AA;
 Query Match 89.0%; Score 1355; DB 22; Length 250;
 Best Local Similarity 100.0%; Pred. No. 7,66-119;
 Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 MRLIQLILALATGIVGETRIIIGFECKPHSQPMQALFERTLLCGATLIAPRWLLTA 92
 DB 1 MRLIQLILALATGIVGETRIIIGFECKPHSQPMQALFERTLLCGATLIAPRWLLTA 60
 QY 93 AHCLKPRYIVHIGQNLKKEGCEQTRATATSPFHGPFNNLSLPNKDHRNDIMLVKMASPV 152
 DB 61 AHCLKPRYIVHIGQNLKKEGCEQTRATATSPFHGPFNNLSLPNKDHRNDIMLVKMASPV 120
 QY 153 SITMAVRPLTSSRCVTAGTSCGISWGSTSSPOLRLPHTLRCAANTITIEHOKENAYPG 212
 DB 121 SITMAVRPLTSSRCVTAGTSCGISWGSTSSPOLRLPHTLRCAANTITIEHOKENAYPG 180
 QY 213 NITDTMVCASVOEGKDCSCGDSGGLVNCNOSLOGIISWGDDPCAITRKPGVYTKVKYV 272
 DB 181 NITDTMVCASVOEGKDCSCGDSGGLVNCNOSLOGIISWGDDPCAITRKPGVYTKVKYV 240
 QY 273 DWIOETMKNN 282
 DB 241 DWIOETMKNN 250
 RESULT 10
 ID ABG61816
 AC ABG61816 standard; Protein; 250 AA.
 XX
 DT 15-AUG-2002 (first entry)
 DE Prostate cancer-associated protein #17.
 XX
 KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic.
 XX
 OS Mammalia.
 XX
 PN WO200230268-A2.
 XX
 PD 18-APR-2002.
 XX
 PF 12-OCT-2001; 2001WO-US32045.
 XX
 PR 13-OCT-2000; 2000US-0687576.
 PR 08-DEC-2000; 2000US-0733288.
 PR 08-DEC-2000; 2000US-0733742.
 PR 24-JAN-2001; 2001US-263957P.
 PR 16-MAR-2001; 2001US-276791P.
 PR 06-MAR-2001; 2001US-276888P.
 PR 06-APR-2001; 2001US-281922P.
 PR 24-APR-2001; 2001US-286214P.
 PR 30-APR-2001; 2001US-0847046.
 PR 04-MAY-2001; 2001US-288589P.
 XX
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 XX
 PI Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
 DR WPI; 2002-471335/50.
 DR N-PSDB; ABK92131.
 XX
 PT Detecting a prostate cancer-associated transcript in a cell in a
 PT patient, useful for diagnosing prostate cancer (PC) or screening
 PT modulators of PC, by determining if prostate cancer-associated genes
 PT are expressed in a prostate tissue -
 XX
 PS Claim 27; Page 314; 436bp; English.
 XX
 CC The present invention relates to methods of detecting a prostate
 CC cancer-associated transcript in a cell from a patient. The method
 CC comprises contacting a biological sample from the patient with
 CC prostate cancer-associated polynucleotides (designated PC genes) that
 CC selectively hybridise to a sequence that is at least 80% identical
 CC to them. The prostate cancer-associated polynucleotide sequences
 CC are differentially expressed in prostate tumour tissue or in

CC prostate cancer and are derived from the tissues of various
 CC organisms such as humans or other mammals (e.g. mice, sheep and dogs).
 CC The methods of the invention are useful for diagnosing and treating
 CC prostate cancer in mammals. The prostate cancer-associated genes are
 CC useful for diagnosing or treating prostate cancer, as well as for
 CC identifying modulators of prostate cancer or agents that inhibit
 CC prostate cancer. The nucleic acid sequences are particularly useful
 CC in gene therapy, as a vaccine or in antisense applications.
 CC ABG61800-ABG61944 represent prostate cancer-associated proteins.

XX Sequence 250 AA:

Query Match 89.0%; Score 1355; DB 23; Length 250;
 Best Local Similarity 100.0%; Pred. No. 7.6e-119;
 Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 MRLQLILALATGLVGETRIIKGFECRPHSQPQALFEKTRLLCGATLIAPRWLTA 92
 DB 1 MRLQLILALATGLVGETRIIKGFECRPHSQPQALFEKTRLLCGATLIAPRWLTA 60
 QY 93 AHCLKRYIVHGOHNLQKEGCEQRTATSESPFHGPNNSLPKDRNDIMLVKASPV 152
 DB 61 AHCLKRYIVHGOHNLQKEGCEQRTATSESPFHGPNNSLPKDRNDIMLVKASPV 120
 QY 153 SITWAVRPLTSSRCYTAGTSCGISGSGTSSPOLRPHTLRCANITIEHOKENAYPG 212
 DB 121 SITWAVRPLTSSRCYTAGTSCGISGSGTSSPOLRPHTLRCANITIEHOKENAYPG 180
 QY 213 NITDTWVCASVQEGKDCQSDSGGLVNCNQLGIIISWGDPICATRRPGVYTKCKYV 272
 DB 181 NITDTWVCASVQEGKDCQSDSGGLVNCNQLGIIISWGDPICATRRPGVYTKCKYV 240
 QY 273 DWIOETMKN 282
 DB 241 DWIOETMKN 250

RESULT 11

AB955526
 ID ABB95526 standard. Protein, 250 AA.

XX ABB95526;
 AC
 XX
 DT 19-JUL-2002 (first entry)
 XX
 DE Human angiogenesis related protein PRO1279 SEQ ID NO: 208.
 XX
 KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
 KW cardiac; cytoskeletal; antiangiogenic; hypotensive; vulnerary;
 KW antiarteriosclerotic.
 XX
 OS Homo sapiens.
 OS
 XX
 PN WO200208284-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 09-JUL-2001; 2001WO-US21735.
 XX
 PR 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 28-JUL-2000; 2000US-220664P.
 PR 02-AUG-2000; 2000WO-US20710.
 PR 17-AUG-2000; 2000US-222695P.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 07-SEP-2000; 2000US-230978P.
 PR 15-SEP-2000; 2000US-000000P.
 PR 18-SEP-2000; 2000US-0664610.
 PR 24-OCT-2000; 2000US-242922P.
 PR

PR 08-NOV-2000; 2000US-0709238.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 22-JAN-2001; 2001US-0767609.
 PR 28-FEB-2001; 2001US-0796498.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0806889.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 30-MAY-2001; 2001US-0870574.
 PR 30-MAY-2001; 2001WO-US17443.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 28-JUN-2001; 2001WO-US00000.

PA (GETH) GENENTECH INC.
 PA (BAKE) BAKER K P.
 PA (FERR) FERRARA N.
 PA (GERB) GERBER H.
 PA (GERR) GERRITSEN M E.
 PA (GODD) GODDARD A.
 PA (GODO) GODOWSKI P J.
 PA (GURN) GURNEY A L.
 PA (HILL) HILLAN K J.
 PA (MARS) MARSTERS S A.
 PA (PANJ) PAN J.
 PA (PAON) PAONI N F.
 PA (STEP) STEPHAN J F.
 PA (WATA) WATANABE C K.
 PA (WILL) WILLIAMS P M.
 PA (WOOD) WOOD W I.

PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
 PI Stephens JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 DR WPI; 2002-171999/22.
 DR N-PSDB; ABL95664.

PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal -
 PS Claim 11; Fig 208; 567bp; English.

XX The present invention provides the protein and coding sequences of human
 CC PRO proteins. These are useful for treating or diagnosing a
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac
 CC hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphoiditis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The present sequence is a PRO protein of the invention.

XX Sequence 250 AA:

Query Match 89.0%; Score 1355; DB 23; Length 250;
 Best Local Similarity 100.0%; Pred. No. 7.6e-119;
 Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 MRLQLILALATGLVGETRIIKGFECRPHSQPQALFEKTRLLCGATLIAPRWLTA 92
 DB 1 MRLQLILALATGLVGETRIIKGFECRPHSQPQALFEKTRLLCGATLIAPRWLTA 60

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DB 61 AHCLKPRYIVH.GOHNLQKEGCEQTRTATESFPHPGFNNSLPKXDRNDIMLVKMASPV 120
OY 153 SITWAVRPLTSSRCVTAGTSCLSISGWSSTSPOLRPLHTRCANITIIIEHOKCENAYPG 212
DB 121 SITWAVRPLTSSRCVTAGTSCLSISGWSSTSPOLRPLHTRCANITIIIEHOKCENAYPG 180
OY 213 NITDTMVCASVQEGKDSGQDGGPGLVCNOSLOGIISWGODPCAITRKPGVYTKVKYV 272
DB 181 NITDTMVCASVQEGKDSGQDGGPGLVCNOSLOGIISWGODPCAITRKPGVYTKVKYV 240
OY 273 DWIOETMKN 282
DB 241 DWIOETMKN 250

RESULT 12
ABB84920
ID ABB84920 standard; Protein: 250 AA.
XX
AC ABB84920;
XX
DE 16-MAY-2002 (first entry)
XX
XX Human PRO1279 protein sequence SEQ ID NO:208.
XX
KW Human; angiogenesis; cardiatic; cytoskeletal; antiangiogenic; hypotensive;
KW vulnerability; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KW age-related macular degeneration; arterial restenosis; angina;
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KW wound healing; chromosome mapping; gene mapping.
XX
OS Homo sapiens.
XX
PN WO200200690-A2.
XX
PD 03-JAN-2002.
XX
XX 20-JUN-2001; 2001WO-US19692.
XX
XX 23-JUN-2000; 2000US-213637P.
XX 20-JUL-2000; 2000US-219556P.
XX 25-JUL-2000; 2000US-220624P.
XX 25-JUL-2000; 2000US-220664P.
XX 28-JUL-2000; 2000WO-US20710.
XX 02-AUG-2000; 2000US-222695P.
XX 17-AUG-2000; 2000US-0643657.
XX 23-AUG-2000; 2000WO-US23522.
XX 07-SEP-2000; 2000US-230978P.
XX 18-SEP-2000; 2000US-066610.
XX 18-SEP-2000; 2000US-0665350.
XX 24-OCT-2000; 2000US-242922P.
XX 08-NOV-2000; 2000US-0709238.
XX 08-NOV-2000; 2000WO-US30952.
XX 10-NOV-2000; 2000WO-US30873.
XX 01-DEC-2000; 2000WO-US32678.
XX 20-DEC-2000; 2000US-0747259.
XX 20-DEC-2000; 2000WO-US34956.
XX 22-JAN-2001; 2001US-0767609.
XX 28-FEB-2001; 2001US-0796498.
XX 28-FEB-2001; 2001WO-US06520.
XX 01-MAR-2001; 2001WO-US06666.
XX 09-MAR-2001; 2001US-0802706.
XX 14-MAR-2001; 2001US-0808689.
XX 22-MAR-2001; 2001US-0816744.
XX 05-APR-2001; 2001US-0828366.
XX 10-MAY-2001; 2001US-0854208.

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PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 25-MAY-2001; 2001WO-US17092.
PR 30-MAY-2001; 2001US-0870574.
PR 30-MAY-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Ferrara N, Gerber H, Gertlsen ME, Goddard A,
XX Godowski PJ, Gueney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
XX Stephan UF, Watanabe CK, Williams FM, Wood WI, Ye W,
XX WPI, 2002-090516/12.
XX N-PSDB; ABL88175.
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
XX useful in diagnosis and treatment of cardiovascular (e.g. myocardial
XX infarction), endothelial or angiogenic disorders in a mammal -
XX
XX Claim 11; Fig 208; 565pp; English.
XX
XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
XX ABB85003. The PRO proteins and polynucleotides have cardiatic, cytoskeletal,
XX antiangiogenic, hypotensive, vulnerability and antiarteriosclerotic
XX activities, and can be used in gene therapy. The PRO polynucleotides,
XX proteins, agonists and antagonists are useful for treating or diagnosing
XX a cardiovascular, endothelial or angiogenic disorder in a mammal,
XX e.g. cardiac hypertrophy, trauma, cancer, age-related macular
XX degeneration, atherosclerosis, hypertension, arterial restenosis,
XX rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
XX lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
XX carcinoma) and wound healing. The PRO polynucleotides have applications
XX in molecular biology, including use as hybridisation probes, and in
XX chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
XX probes used in the exemplification of the present invention.
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XX SQ Sequence 250 AA;
XX
XX Query Match 89.0%; Score 1355; DB 23; Length 250;
XX Best Local Similarity 100.0%; Pred. No. 7,6e-119;
XX Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MRLIQLIALATGLVGETRIIKGFCKPHSQWQALFEKTRLLCGATLIAPRWLITA 60
OY 93 AHCLKPRYIVH.GOHNLQKEGCEQTRTATESFPHPGFNNSLPKXDRNDIMLVKMASPV 152
DB 61 AHCLKPRYIVH.GOHNLQKEGCEQTRTATESFPHPGFNNSLPKXDRNDIMLVKMASPV 120
OY 153 SITWAVRPLTSSRCVTAGTSCLSISGWSSTSPOLRPLHTRCANITIIIEHOKCENAYPG 212
DB 121 SITWAVRPLTSSRCVTAGTSCLSISGWSSTSPOLRPLHTRCANITIIIEHOKCENAYPG 180
OY 213 NITDTMVCASVQEGKDSGQDGGPGLVCNOSLOGIISWGODPCAITRKPGVYTKVKYV 272
DB 181 NITDTMVCASVQEGKDSGQDGGPGLVCNOSLOGIISWGODPCAITRKPGVYTKVKYV 240
OY 273 DWIOETMKN 282
DB 241 DWIOETMKN 250

RESULT 13
AAU83684
ID AAU83684 standard; Protein: 250 AA.
XX
AC AAU83684;
XX
XX 08-MAY-2002 (first entry)
XX
XX

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PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28403.
PR 01-DEC-1999; 99WO-US28501.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28851.
PR 02-DEC-1999; 99WO-US28854.
PR 02-DEC-1999; 99WO-US28855.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 22-DEC-1999; 99WO-US30999.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05746.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 22-JUN-2001; 2001WO-US20116.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 20-DEC-2000; 2000WO-US21735.
PR 28-FEB-2001; 2001US-0796498.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 18-MAY-2001; 2001US-0860216.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 21-JUN-2001; 2001US-0887879.
PR 18-JUL-2001; 2001US-0908827.
PR 06-AUG-2001; 2001US-0924419.
PR 09-AUG-2001; 2001US-0927966.
PR 16-AUG-2001; 2001US-0931836.
PR 19-DEC-2001; 2001US-0028072.
XX

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PA (GETH ) GENENTECH INC.
XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
PI Gertelsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX MPI: 2003-332040/31.
DR N-PSDB; ACD03855.
DR
XX New secreted and transmembrane PRO nucleic acids, useful for gene
PT therapy, in chromosome and gene mapping, as chromosome markers, in
PT tissue typing, and in chromosome identification
XX
PS Claim 12; Fig 506; 660pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The
CC PRO polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for
CC linking bioactive molecules to cells expressing PRO polypeptides,
CC for modulating biological activities of cells expressing PRO
CC polypeptides, and for identifying agonists or antagonists.
CC The PRO polypeptides are useful for stimulating the release of
CC tumour necrosis factor (TNF)-alpha from human blood, for stimulating
CC the proliferation or differentiation of chondrocytes, and detecting the
CC presence of tumours. The polynucleotide sequences encoding PRO
CC polypeptides are useful as hybridisation probes, in chromosome and
CC gene mapping, in the generation of antisense RNA and DNA, in the
CC preparation of PRO polypeptides, for generating transgenic animals or
CC knockout animals, for the genetic analysis of individuals with genetic
CC disorders, and in gene therapy. ABU6570-ABU6684 represent the human
CC PRO polypeptides of the invention.
CC Note: The sequence data for this patent was obtained in electronic
CC format directly from the USPTO web site at
CC seqdata.uspto.gov/patseq/idententry.html.
XX
SQ Sequence 250 AA;
XX
XX Query Match 89.0%; Score 1355; DB 24; Length 250;
XX Best Local Similarity 100.0%; Pred. No. 7,6e-119;
XX Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 33 MRLQLILALATNGGERRIINGEFCCKPSPQWQALPEKPTLLGCATLIARMLLTA 92
DB 1 MRLQLILALATLVGEGTRIINGEFCCKPSPQWQALPEKPTLLGCATLIARMLLTA 60
QY 93 AHCLKPRIVYVHLGQHNLOKEGCEGQRTATSFPHGFNNSLPKDHRNDIMLVKMASPV 152
DB 61 AHCLKPRIVYVHLGQHNLOKEGCEGQRTATSFPHGFNNSLPKDHRNDIMLVKMASPV 120
QY 153 SITWAVRPLTISRCAVTAAGTSLISGSGTSSPOLRLPHTLRCAVITIIHOKCENAVPG 212
DB 121 SITWAVRPLTISRCAVTAAGTSLISGSGTSSPOLRLPHTLRCAVITIIHOKCENAVPG 180
QY 213 NITPTWVCASVOEGCKSCCGDSGGLVNCOSLOGITISWQDPCAIRRKGVYTKVKYV 272
DB 181 NITPTWVCASVOEGCKSCCGDSGGLVNCOSLOGITISWQDPCAIRRKGVYTKVKYV 240
QY 273 DWIOETMKNK 282
DB 241 DWIOETMKNK 250
XX
RESULT 15
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ID ABU67098 standard; Protein; 250 AA.
XX
AC ABU67098;
XX
XX 27-MAY-2003 (first entry)
XX
XX Human secreted/transmembrane, PRO, protein SEQ ID 506.
XX

```

KW Human; secreted protein; transmembrane protein; PRO;
 KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;
 KW infertility; birth defects; premature aging; AIDS; biosensor;
 KW acquired immunodeficiency syndrome; cancer; diabetic complication;
 KW bioreactor; tumour.
 XX
 OS Homo sapiens.
 PN US2003032155-A1.
 XX
 PD 13-FEB-2003.
 XX
 PF 03-MAY-2002; 2002US-0137865.
 XX
 PR 31-MAR-1997; 97WO-US05230.
 PR 12-JUN-1998; 98WO-US12456.
 PR 14-JUL-1998; 98WO-US14552.
 PR 28-AUG-1998; 98WO-US17888.
 PR 10-SEP-1998; 98WO-US18824.
 PR 14-SEP-1998; 98WO-US19093.
 PR 14-SEP-1998; 98WO-US19094.
 PR 14-SEP-1998; 98WO-US19177.
 PR 16-SEP-1998; 98WO-US19330.
 PR 17-SEP-1998; 98WO-US19437.
 PR 07-OCT-1998; 98WO-US21141.
 PR 29-OCT-1998; 98WO-US22991.
 PR 20-NOV-1998; 98WO-US24855.
 PR 01-DEC-1998; 98WO-US25106.
 PR 05-JAN-1999; 99WO-US00106.
 PR 08-MAR-1999; 99WO-US05028.
 PR 10-MAR-1999; 99WO-US05190.
 PR 20-APR-1999; 99WO-US08615.
 PR 14-MAY-1999; 99WO-US10733.
 PR 02-JUN-1999; 99WO-US12252.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20944.
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 PR 15-SEP-1999; 99WO-US21547.
 PR 05-OCT-1999; 99WO-US23089.
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 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
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 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
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 PR 10-MAR-2000; 2000WO-US05841.
 PR 15-MAR-2000; 2000WO-US06319.
 PR 20-MAR-2000; 2000WO-US06884.
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 PR 17-MAY-2000; 2000WO-US08439.
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PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
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 PR 23-AUG-2000; 2000WO-US23522.
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 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 22-JUN-2001; 2001WO-US20116.
 PR 29-JUN-2001; 2001WO-US21066.
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 PR 20-DEC-2000; 2000US-0747259.
 PR 28-FEB-2001; 2001US-0796498.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0808689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 18-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001US-0860216.
 PR 25-MAY-2001; 2001US-0866028.
 PR 01-JUN-2001; 2001US-0866034.
 PR 05-JUN-2001; 2001US-0872035.
 PR 14-JUN-2001; 2001US-0874503.
 PR 19-JUN-2001; 2001US-0882636.
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 PR 09-AUG-2001; 2001US-0927796.
 PR 16-AUG-2001; 2001US-0931836.
 PR 19-DEC-2001; 2001US-0028072.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W,
 Geritsen ME, Goddard A, Godowski PJ, Gunney AL, Sherwood S,
 Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR MPI; 2003-331925/31.
 XX
 PS N-PSDB; ACN04276.
 XX
 PT New secreted and transmembrane nucleic acids and polypeptides,
 designated as PRO, useful for treating inflammation, organ failure,
 atherosclerosis, cardiac injury, infertility, birth defects, premature
 aging, AIDS, or cancer -
 PT
 PR
 XX
 PS Claim 12, Fig 506; 659pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising, or which is
 CC at least 80% identical to, or the full-length coding sequence of, any of
 CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
 CC (one of 275 secreted or transmembrane proteins). The nucleic acid
 CC further comprises the full-length coding sequence of the DNA deposited
 CC under American Type Culture Collection (ATCC) accession number in a list
 CC given in the specification. Also included are vectors and host
 CC cells for producing PRO proteins, PRO fusion proteins, anti-PRO
 CC antibodies, PRO extracellular domains and mature sequences, methods
 CC of detecting PRO proteins, methods for stimulating the release of
 CC TNF-alpha (tumour necrosis factor alpha) from human blood,
 CC (and the proliferation of differentiation of chondrocyte cells, the
 CC proliferation of, or gene expression in pericyte cells, the release or
 CC proteoglycans from cartilage, proliferation of inner ear utricular
 CC supporting cells, the proliferation of T-lymphocyte cells, the release
 CC of a cytokine from peripheral blood mononuclear cells (PBMC), or the

CC proliferation of endothelial cells), a method for modulating the uptake
 CC of glucose or free fatty acid (FFA) by skeletal muscle cells,
 CC a method for inhibiting the binding of A-peptide to factor VIIA,
 CC or the differentiation of adipocyte cells, a method for detecting the
 CC presence of a tumor in a mammal and an oligonucleotide probe derived
 CC from any of the nucleotide sequences cited above. The nucleic acids and
 CC polypeptides are useful for treating inflammatory diseases, organ
 CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
 CC premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or
 CC diabetic complications. The nucleic acids are useful as hybridisation
 CC probes, in chromosome and gene mapping, and in generating antisense RNA
 CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,
 CC biosensors or bioreactors. Both are useful in tissue typing.
 CC The present sequence represents a PRO protein of the invention.

XX Sequence 250 AA;

Query Match 89.0%; Score 1355; DB 24; Length 250;
 Best Local Similarity 100.0%; Pred No. 7.6e-119;
 Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	1	MRILQILILALATGLVGEFTRIIKGFECKPHSQPMQALFEKTRLLCGATLLAPRWLTA	60
QY	93	AHCLKPRYIVHLGQHNLOKEGCEQTRTATESFPHPGFNNSLPNKDRNDIMLVKMASPV	152
DB	61	AHCLKPRYIVHLGQHNLOKEGCEQTRTATESFPHPGFNNSLPNKDRNDIMLVKMASPV	120
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DB	121	SITWVRPLTSLSPRCVTAGTSCGISGSGTSSPOLRLPHTLRCAANTTIEHOKCENAYPG	180
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DB	181	NITDTMVCASVOEGGKDCSQGDSGGPLVNCNGLGIIISWGDPCAITRRKGVYTRVCKYV	240
QY	273	DWIOETMKNN 282	
DB	241	DWIOETMKNN 250	

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GenCore version 5.1.6
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OM protein - protein search, using sw model

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(without alignments)
1746.375 Million cell updates/sec

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Post-processing: Minimum Match 0%

Maximum Match 100%

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- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1355	89.0	250	11	US-09-946-374-170 Sequence 170, App
2	1355	89.0	250	12	US-10-015-387A-170 Sequence 170, App
3	1355	89.0	250	12	US-10-137-870-506 Sequence 506, App
4	1355	89.0	250	12	US-10-140-018-506 Sequence 506, App
5	1355	89.0	250	12	US-10-140-021-506 Sequence 506, App
6	1355	89.0	250	12	US-10-140-024-506 Sequence 506, App
7	1355	89.0	250	12	US-10-140-471-506 Sequence 506, App
8	1355	89.0	250	12	US-10-140-807-506 Sequence 506, App
9	1355	89.0	250	12	US-10-140-922-506 Sequence 506, App
10	1355	89.0	250	12	US-10-140-924-506 Sequence 506, App
11	1355	89.0	250	12	US-10-140-926-506 Sequence 506, App
12	1355	89.0	250	12	US-10-141-698-506 Sequence 506, App
13	1355	89.0	250	12	US-10-141-702-506 Sequence 506, App
14	1355	89.0	250	12	US-10-141-704-506 Sequence 506, App
15	1355	89.0	250	12	US-10-142-421-506 Sequence 506, App

16	1355	89.0	250	12	US-10-142-432-506 Sequence 506, App
17	1355	89.0	250	12	US-10-142-767-506 Sequence 506, App
18	1355	89.0	250	12	US-10-143-033-506 Sequence 506, App
19	1355	89.0	250	12	US-10-144-994-506 Sequence 506, App
20	1355	89.0	250	12	US-10-145-628-506 Sequence 506, App
21	1355	89.0	250	12	US-10-145-631-506 Sequence 506, App
22	1355	89.0	250	12	US-10-145-633-506 Sequence 506, App
23	1355	89.0	250	12	US-10-145-746-506 Sequence 506, App
24	1355	89.0	250	12	US-10-145-748-506 Sequence 506, App
25	1355	89.0	250	12	US-10-145-823-506 Sequence 506, App
26	1355	89.0	250	12	US-10-145-826-506 Sequence 506, App
27	1355	89.0	250	12	US-10-145-870-506 Sequence 506, App
28	1355	89.0	250	12	US-10-145-876-506 Sequence 506, App
29	1355	89.0	250	12	US-10-145-959-506 Sequence 506, App
30	1355	89.0	250	12	US-10-146-724-506 Sequence 506, App
31	1355	89.0	250	12	US-10-146-725-506 Sequence 506, App
32	1355	89.0	250	12	US-10-146-795-506 Sequence 506, App
33	1355	89.0	250	12	US-10-147-495-506 Sequence 506, App
34	1355	89.0	250	12	US-10-147-501-506 Sequence 506, App
35	1355	89.0	250	12	US-10-147-504-506 Sequence 506, App
36	1355	89.0	250	12	US-10-147-506-506 Sequence 506, App
37	1355	89.0	250	12	US-10-147-509-506 Sequence 506, App
38	1355	89.0	250	12	US-10-147-510-506 Sequence 506, App
39	1355	89.0	250	12	US-10-147-511-506 Sequence 506, App
40	1355	89.0	250	12	US-10-147-529-506 Sequence 506, App
41	1355	89.0	250	12	US-10-152-397-506 Sequence 506, App
42	1355	89.0	250	12	US-10-153-586-506 Sequence 506, App
43	1355	89.0	250	12	US-10-158-783-506 Sequence 506, App
44	1355	89.0	250	12	US-10-158-786-506 Sequence 506, App
45	1355	89.0	250	12	US-10-006-130A-170 Sequence 170, App

ALIGNMENTS

RESULT 1

US-09-946-374-170

Sequence 170, Application US/09946374

Publicatoin No. US20030073129A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Bortstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2830P1C1

CURRENT APPLICATION NUMBER: US/09/946.374

CURRENT FILING DATE: 2001-09-04

PRIOR APPLICATION NUMBER: 60/098716

PRIOR FILING DATE: 1998-09-01

PRIOR APPLICATION NUMBER: 60/098723

PRIOR FILING DATE: 1998-09-01

PRIOR APPLICATION NUMBER: 60/098749

PRIOR FILING DATE: 1998-09-01

PRIOR APPLICATION NUMBER: 60/098750

[illegible]

1	PRIOR APPLICATION NUMBER: 60/101471
2	PRIOR FILING DATE: 1998-09-23
3	PRIOR APPLICATION NUMBER: 60/101472
4	PRIOR FILING DATE: 1998-09-23
5	PRIOR APPLICATION NUMBER: 60/101474
6	PRIOR FILING DATE: 1998-09-23
7	PRIOR APPLICATION NUMBER: 60/101475
8	PRIOR FILING DATE: 1998-09-23
9	PRIOR APPLICATION NUMBER: 60/101476
10	PRIOR FILING DATE: 1998-09-23
11	PRIOR APPLICATION NUMBER: 60/101477
12	PRIOR FILING DATE: 1998-09-23
13	PRIOR APPLICATION NUMBER: 60/101479
14	PRIOR FILING DATE: 1998-09-23
15	PRIOR APPLICATION NUMBER: 60/101738
16	PRIOR FILING DATE: 1998-09-24
17	PRIOR APPLICATION NUMBER: 60/101741
18	PRIOR FILING DATE: 1998-09-24
19	PRIOR APPLICATION NUMBER: 60/101743
20	PRIOR FILING DATE: 1998-09-24
21	PRIOR APPLICATION NUMBER: 60/101915
22	PRIOR FILING DATE: 1998-09-24
23	PRIOR APPLICATION NUMBER: 60/101916
24	PRIOR FILING DATE: 1998-09-24
25	PRIOR APPLICATION NUMBER: 60/102207
26	PRIOR FILING DATE: 1998-09-29
27	PRIOR APPLICATION NUMBER: 60/102240
28	PRIOR FILING DATE: 1998-09-29
29	PRIOR APPLICATION NUMBER: 60/102307
30	PRIOR FILING DATE: 1998-09-29
31	PRIOR APPLICATION NUMBER: 60/102330
32	PRIOR FILING DATE: 1998-09-29
33	PRIOR APPLICATION NUMBER: 60/102331
34	PRIOR FILING DATE: 1998-09-29
35	PRIOR APPLICATION NUMBER: 60/102484
36	PRIOR FILING DATE: 1998-09-30
37	PRIOR APPLICATION NUMBER: 60/102487
38	PRIOR FILING DATE: 1998-09-30
39	PRIOR APPLICATION NUMBER: 60/102570
40	PRIOR FILING DATE: 1998-09-30
41	PRIOR APPLICATION NUMBER: 60/102571
42	PRIOR FILING DATE: 1998-09-30
43	PRIOR APPLICATION NUMBER: 60/102684
44	PRIOR FILING DATE: 1998-10-01
45	PRIOR APPLICATION NUMBER: 60/102687
46	PRIOR FILING DATE: 1998-10-01
47	PRIOR APPLICATION NUMBER: 60/102965
48	PRIOR FILING DATE: 1998-10-02
49	PRIOR APPLICATION NUMBER: 60/103258
50	PRIOR FILING DATE: 1998-10-06
51	PRIOR APPLICATION NUMBER: 60/103314
52	PRIOR FILING DATE: 1998-10-07
53	PRIOR APPLICATION NUMBER: 60/103315
54	PRIOR FILING DATE: 1998-10-07
55	PRIOR APPLICATION NUMBER: 60/103328
56	PRIOR FILING DATE: 1998-10-07
57	PRIOR APPLICATION NUMBER: 60/103355
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61	PRIOR APPLICATION NUMBER: 60/103401
62	PRIOR FILING DATE: 1998-10-07
63	PRIOR APPLICATION NUMBER: 60/103449
64	PRIOR FILING DATE: 1998-10-08
65	PRIOR APPLICATION NUMBER: 60/103679
66	PRIOR FILING DATE: 1998-10-08
67	PRIOR APPLICATION NUMBER: 60/103711
68	PRIOR FILING DATE: 1998-10-08
69	PRIOR APPLICATION NUMBER: 60/104257
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92	PRIOR FILING DATE: 1998-10-08
93	PRIOR APPLICATION NUMBER: 60/104257
94	PRIOR FILING DATE: 1998-10-08
95	PRIOR APPLICATION NUMBER: 60/104257
96	PRIOR FILING DATE: 1998-10-08
97	PRIOR APPLICATION NUMBER: 60/104257
98	PRIOR FILING DATE: 1998-10-08
99	PRIOR APPLICATION NUMBER: 60/104257
100	PRIOR FILING DATE: 1998-10-08


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; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807

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Query Match      89.0%; Score 1355; DB 11; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 33 MRILQILILALATGIVGSETRIIKGFECCKPHSQPQWALFEKTRLLCGATLLAPRWLLTA 92
DB 1 MRILQILILALATGIVGSETRIIKGFECCKPHSQPQWALFEKTRLLCGATLLAPRWLLTA 60
QY 93 AHCLKPRYIVHLGQHNLOKEEGCEQTRTATESFPHGFNNSLPNKDRNDIMLVKASPV 152
DB 61 AHCLKPRYIVHLGQHNLOKEEGCEQTRTATESFPHGFNNSLPNKDRNDIMLVKASPV 120
QY 153 SITMAVRPLTSSRCVTAGTSCISGWSSTSPQRLPPTLRCANTITIEHOKCENAYPG 212
DB 121 SITMAVRPLTSSRCVTAGTSCISGWSSTSPQRLPPTLRCANTITIEHOKCENAYPG 180
QY 213 NITDVMCASVOEGKDSQGDSPGVNOSLOGIISWGDPICATTRKPGVYTKCKYV 272
DB 181 NITDVMCASVOEGKDSQGDSPGVNOSLOGIISWGDPICATTRKPGVYTKCKYV 240
QY 273 DWIOETMKNN 282
DB 241 DWIOETMKNN 250

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RESULT 2

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US-10-015-387A-170
; Sequence 170, Application US/10015387A
; Publication No. US20030135034A1
; GENERAL INFORMATION:

```

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; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC54
; CURRENT APPLICATION NUMBER: US/10/015,387A
; CURRENT FILING DATE: 2001-12-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 170
; LENGTH: 250
; TYPE: PRT

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; ORGANISM: Homo sapiens
US-10-015-387A-170

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Query Match      89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 33 MRILQILILALATGIVGSETRIIKGFECCKPHSQPQWALFEKTRLLCGATLLAPRWLLTA 92
DB 1 MRILQILILALATGIVGSETRIIKGFECCKPHSQPQWALFEKTRLLCGATLLAPRWLLTA 60
QY 93 AHCLKPRYIVHLGQHNLOKEEGCEQTRTATESFPHGFNNSLPNKDRNDIMLVKASPV 152
DB 61 AHCLKPRYIVHLGQHNLOKEEGCEQTRTATESFPHGFNNSLPNKDRNDIMLVKASPV 120
QY 153 SITMAVRPLTSSRCVTAGTSCISGWSSTSPQRLPPTLRCANTITIEHOKCENAYPG 212
DB 121 SITMAVRPLTSSRCVTAGTSCISGWSSTSPQRLPPTLRCANTITIEHOKCENAYPG 180
QY 213 NITDVMCASVOEGKDSQGDSPGVNOSLOGIISWGDPICATTRKPGVYTKCKYV 272
DB 181 NITDVMCASVOEGKDSQGDSPGVNOSLOGIISWGDPICATTRKPGVYTKCKYV 240
QY 273 DWIOETMKNN 282
DB 241 DWIOETMKNN 250

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RESULT 3

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US-10-137-870-506
; Sequence 506, Application US/10137870
; Publication No. US20030138883A1
; GENERAL INFORMATION:

```

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; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC155
; CURRENT APPLICATION NUMBER: US/10/137,870
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-870-506

```

```

Query Match      89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 33 MRILQILILALATGIVGSETRIIKGFECCKPHSQPQWALFEKTRLLCGATLLAPRWLLTA 92
DB 1 MRILQILILALATGIVGSETRIIKGFECCKPHSQPQWALFEKTRLLCGATLLAPRWLLTA 60
QY 93 AHCLKPRYIVHLGQHNLOKEEGCEQTRTATESFPHGFNNSLPNKDRNDIMLVKASPV 152

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Db      61 AHCLKPRYIVHLGQHNLOKEGCEQTRTATESFPHGPFNNSLPNKDHNDIMLVKMASPV 120
QY      153 SITWAVRPLTSSRCVTAGTSCGISGSGTSSPOLRLPHTLRCAITIIIEHOKCENAYPG 212
Db      121 SITWAVRPLTSSRCVTAGTSCGISGSGTSSPOLRLPHTLRCAITIIIEHOKCENAYPG 180
QY      213 NITDPMVCAVQEGGKSCQDGGSPPLVCNOSLOGIISWGDPCAITRKPGVYTKVCKYV 272
Db      181 NITDPMVCAVQEGGKSCQDGGSPPLVCNOSLOGIISWGDPCAITRKPGVYTKVCKYV 240
QY      273 DWIOETMKNN 282
Db      241 DWIOETMKNN 250

RESULT 4
US-10-140-018-506
; Sequence 506, Application US/10140018
; Publication No. US20030138865A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C158
; CURRENT APPLICATION NUMBER: US/10/140,018
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-018-506

Query Match      89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1,3e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      33 MRLIQLILALATGIVGSETRIIKGFECCKPHSQPQWALFEXTRLGCAITLIARWLTA 92
Db      1 MRLIQLILALATGIVGSETRIIKGFECCKPHSQPQWALFEXTRLGCAITLIARWLTA 60
QY      93 AHCLKPRYIVHLGQHNLOKEGCEQTRTATESFPHGPFNNSLPNKDHNDIMLVKMASPV 152
Db      61 AHCLKPRYIVHLGQHNLOKEGCEQTRTATESFPHGPFNNSLPNKDHNDIMLVKMASPV 120
QY      153 SITWAVRPLTSSRCVTAGTSCGISGSGTSSPOLRLPHTLRCAITIIIEHOKCENAYPG 212
Db      121 SITWAVRPLTSSRCVTAGTSCGISGSGTSSPOLRLPHTLRCAITIIIEHOKCENAYPG 180
QY      213 NITDPMVCAVQEGGKSCQDGGSPPLVCNOSLOGIISWGDPCAITRKPGVYTKVCKYV 272
Db      181 NITDPMVCAVQEGGKSCQDGGSPPLVCNOSLOGIISWGDPCAITRKPGVYTKVCKYV 240
QY      273 DWIOETMKNN 282
Db      241 DWIOETMKNN 250
```

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RESULT 5
US-10-140-021-506
; Sequence 506, Application US/10140021
; Publication No. US20030138866A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C167
; CURRENT APPLICATION NUMBER: US/10/140,021
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-021-506

Query Match      89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1,3e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      33 MRLIQLILALATGIVGSETRIIKGFECCKPHSQPQWALFEXTRLGCAITLIARWLTA 92
Db      1 MRLIQLILALATGIVGSETRIIKGFECCKPHSQPQWALFEXTRLGCAITLIARWLTA 60
QY      93 AHCLKPRYIVHLGQHNLOKEGCEQTRTATESFPHGPFNNSLPNKDHNDIMLVKMASPV 152
Db      61 AHCLKPRYIVHLGQHNLOKEGCEQTRTATESFPHGPFNNSLPNKDHNDIMLVKMASPV 120
QY      153 SITWAVRPLTSSRCVTAGTSCGISGSGTSSPOLRLPHTLRCAITIIIEHOKCENAYPG 212
Db      121 SITWAVRPLTSSRCVTAGTSCGISGSGTSSPOLRLPHTLRCAITIIIEHOKCENAYPG 180
QY      213 NITDPMVCAVQEGGKSCQDGGSPPLVCNOSLOGIISWGDPCAITRKPGVYTKVCKYV 272
Db      181 NITDPMVCAVQEGGKSCQDGGSPPLVCNOSLOGIISWGDPCAITRKPGVYTKVCKYV 240
QY      273 DWIOETMKNN 282
Db      241 DWIOETMKNN 250

RESULT 6
US-10-140-274-506
; Sequence 506, Application US/10140274
; Publication No. US20030143674A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
```

```

; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C163
; CURRENT APPLICATION NUMBER: US/10/140,471
; PRIOR APPLICATION: 2002-05-06
; NUMBER OF SEQ ID NOS: 550
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-471-506

Query Match      89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 MIIQLIILALATGLVGETRIIIGKECKPHSQPQMAALFEKTRLLCGATLIIAPRWLTA 92
Db 1 MIIQLIILALATGLVGETRIIIGKECKPHSQPQMAALFEKTRLLCGATLIIAPRWLTA 60

QY 93 AHCLKPRYIVHLGOHNLQKEGCEOTRTATESFPHGFNNSLPNKDRNDIMLVKMASPV 152
Db 61 AHCLKPRYIVHLGOHNLQKEGCEOTRTATESFPHGFNNSLPNKDRNDIMLVKMASPV 120

QY 153 SITMAVRPLTSSRCVTAGTSCSLISGWGSTSSPOLRLPHTLRCANITIIIEHOKCENAYPG 212
Db 121 SITMAVRPLTSSRCVTAGTSCSLISGWGSTSSPOLRLPHTLRCANITIIIEHOKCENAYPG 180

QY 213 NITDTMVCASVOEGKDCSQGDSGGLVNCOSLQGIISWGODPCAITRRKPGVYTVCKXV 272
Db 181 NITDTMVCASVOEGKDCSQGDSGGLVNCOSLQGIISWGODPCAITRRKPGVYTVCKXV 240

QY 273 DWIETMKNN 282
Db 241 DWIETMKNN 250

RESULT 7
US-10-140-471-506
; Sequence 506, Application US/10140471
; Publication No. US20030138887A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
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; FILE REFERENCE: P3330R1C163
; CURRENT APPLICATION NUMBER: US/10/140,471
; PRIOR APPLICATION: 2002-05-06
; NUMBER OF SEQ ID NOS: 550
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-471-506

Query Match      89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 MIIQLIILALATGLVGETRIIIGKECKPHSQPQMAALFEKTRLLCGATLIIAPRWLTA 92
Db 1 MIIQLIILALATGLVGETRIIIGKECKPHSQPQMAALFEKTRLLCGATLIIAPRWLTA 60

QY 93 AHCLKPRYIVHLGOHNLQKEGCEOTRTATESFPHGFNNSLPNKDRNDIMLVKMASPV 152
Db 61 AHCLKPRYIVHLGOHNLQKEGCEOTRTATESFPHGFNNSLPNKDRNDIMLVKMASPV 120

QY 153 SITMAVRPLTSSRCVTAGTSCSLISGWGSTSSPOLRLPHTLRCANITIIIEHOKCENAYPG 212
Db 121 SITMAVRPLTSSRCVTAGTSCSLISGWGSTSSPOLRLPHTLRCANITIIIEHOKCENAYPG 180

QY 213 NITDTMVCASVOEGKDCSQGDSGGLVNCOSLQGIISWGODPCAITRRKPGVYTVCKXV 272
Db 181 NITDTMVCASVOEGKDCSQGDSGGLVNCOSLQGIISWGODPCAITRRKPGVYTVCKXV 240

QY 273 DWIETMKNN 282
Db 241 DWIETMKNN 250

RESULT 8
US-10-140-807-506
; Sequence 506, Application US/10140807
; Publication No. US20030134354A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C174
; CURRENT APPLICATION NUMBER: US/10/140,807
; PRIOR APPLICATION: 2002-05-07
; NUMBER OF SEQ ID NOS: 550
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-807-506

Query Match      89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e-126;
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Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 MRLIQLLLALATGLVGETRIIKGFECCKPHSQPQOALFEKTRLLCGATLIAPRWLLTA 92
DB 1 MRLIQLLLALATGLVGETRIIKGFECCKPHSQPQOALFEKTRLLCGATLIAPRWLLTA 60

QY 93 AHCLKPRYIVHGLGQHNLOKEBCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPV 152
DB 61 AHCLKPRYIVHGLGQHNLOKEBCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPV 120

QY 153 SITWAVRPLTSSRCVTAGTSCGISGWSSTSSPOLRPHLTRCANITIIIEHOKCENAYPG 212
DB 121 SITWAVRPLTSSRCVTAGTSCGISGWSSTSSPOLRPHLTRCANITIIIEHOKCENAYPG 180

QY 213 NITDTMCASVOEGKSCQGDGSGPLVCNOSLOGIISWGODPCAITRKPGVYTKVKYV 272
DB 181 NITDTMCASVOEGKSCQGDGSGPLVCNOSLOGIISWGODPCAITRKPGVYTKVKYV 240

QY 273 DMIOETMKN 282
DB 241 DMIOETMKN 250

RESULT 9

US-10-140-922-506
; Sequence 506, Application US/10140922
; Publication No. US20030138889A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C179
CURRENT APPLICATION NUMBER: US/10/140,922
CURRENT FILING DATE: 2002-05-07
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 506
LENGTH: 250
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-922-506

Query Match 89.0%; Score 1355; DB 12; Length 250;

Best Local Similarity 100.0%; Pred. No. 1,3e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 MRLIQLLLALATGLVGETRIIKGFECCKPHSQPQOALFEKTRLLCGATLIAPRWLLTA 92
DB 1 MRLIQLLLALATGLVGETRIIKGFECCKPHSQPQOALFEKTRLLCGATLIAPRWLLTA 60

QY 93 AHCLKPRYIVHGLGQHNLOKEBCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPV 152
DB 61 AHCLKPRYIVHGLGQHNLOKEBCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPV 120

QY 153 SITWAVRPLTSSRCVTAGTSCGISGWSSTSSPOLRPHLTRCANITIIIEHOKCENAYPG 212
DB 121 SITWAVRPLTSSRCVTAGTSCGISGWSSTSSPOLRPHLTRCANITIIIEHOKCENAYPG 180

QY 213 NITDTMCASVOEGKSCQGDGSGPLVCNOSLOGIISWGODPCAITRKPGVYTKVKYV 272
DB 181 NITDTMCASVOEGKSCQGDGSGPLVCNOSLOGIISWGODPCAITRKPGVYTKVKYV 240

QY 273 DMIOETMKN 282
DB 241 DMIOETMKN 250

RESULT 10

US-10-140-924-506
; Sequence 506, Application US/10140924
; Publication No. US20030134355A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C177
CURRENT APPLICATION NUMBER: US/10/140,924
CURRENT FILING DATE: 2002-05-07
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 506
LENGTH: 250
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-924-506

Query Match 89.0%; Score 1355; DB 12; Length 250;

Best Local Similarity 100.0%; Pred. No. 1,3e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 MRLIQLLLALATGLVGETRIIKGFECCKPHSQPQOALFEKTRLLCGATLIAPRWLLTA 92
DB 1 MRLIQLLLALATGLVGETRIIKGFECCKPHSQPQOALFEKTRLLCGATLIAPRWLLTA 60

QY 93 AHCLKPRYIVHGLGQHNLOKEBCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPV 152
DB 61 AHCLKPRYIVHGLGQHNLOKEBCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPV 120

QY 213 NITDTMCASVOEGKSCQGDGSGPLVCNOSLOGIISWGODPCAITRKPGVYTKVKYV 272
DB 181 NITDTMCASVOEGKSCQGDGSGPLVCNOSLOGIISWGODPCAITRKPGVYTKVKYV 240

QY 273 DMIOETMKN 282
DB 241 DMIOETMKN 250

RESULT 11

US-10-140-926-506
; Sequence 506, Application US/10140926

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Publication No. US20030134356A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C187
CURRENT APPLICATION NUMBER: US/10/140,926
CURRENT FILING DATE: 2002-05-07
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 506
LENGTH: 250
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-926-506

Query Match      89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 33 MRLQLLLALATGLVGETRIIKGFECCKPHSQPQAALEFETRLLCGATLLIAPRWLLTA 92
DB 1 MRLQLLLALATGLVGETRIIKGFECCKPHSQPQAALEFETRLLCGATLLIAPRWLLTA 60
QY 93 AHCLKPRYIVHLGQHNLOKEGCEQRTATSFPHPGFNNSLPNKDHRNDIMLVKMASPV 152
DB 61 AHCLKPRYIVHLGQHNLOKEGCEQRTATSFPHPGFNNSLPNKDHRNDIMLVKMASPV 120
QY 153 SITWAVRPLTSSRCVTAGTSCLSISGWSSTSPQRLPHTLRCAITIIIEHOKCENAYPG 212
DB 121 SITWAVRPLTSSRCVTAGTSCLSISGWSSTSPQRLPHTLRCAITIIIEHOKCENAYPG 180
QY 213 NITDTMVCASVOEGGKDSQCGDSGGLVNCNLSQGIISWGDDPCAITRKPGVYTVCKYV 272
DB 181 NITDTMVCASVOEGGKDSQCGDSGGLVNCNLSQGIISWGDDPCAITRKPGVYTVCKYV 240
QY 273 DWIOETMKNN 282
DB 241 DWIOETMKNN 250

RESULT 12
US-10-141-698-506
Sequence 506, Application US/10141698
Publication No. US20030134357A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
```

```
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C206
CURRENT APPLICATION NUMBER: US/10/141,698
CURRENT FILING DATE: 2002-05-08
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 506
LENGTH: 250
TYPE: PRT
ORGANISM: Homo Sapien
US-10-141-698-506

Query Match      89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.3e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 33 MRLQLLLALATGLVGETRIIKGFECCKPHSQPQAALEFETRLLCGATLLIAPRWLLTA 92
DB 1 MRLQLLLALATGLVGETRIIKGFECCKPHSQPQAALEFETRLLCGATLLIAPRWLLTA 60
QY 93 AHCLKPRYIVHLGQHNLOKEGCEQRTATSFPHPGFNNSLPNKDHRNDIMLVKMASPV 152
DB 61 AHCLKPRYIVHLGQHNLOKEGCEQRTATSFPHPGFNNSLPNKDHRNDIMLVKMASPV 120
QY 153 SITWAVRPLTSSRCVTAGTSCLSISGWSSTSPQRLPHTLRCAITIIIEHOKCENAYPG 212
DB 121 SITWAVRPLTSSRCVTAGTSCLSISGWSSTSPQRLPHTLRCAITIIIEHOKCENAYPG 180
QY 213 NITDTMVCASVOEGGKDSQCGDSGGLVNCNLSQGIISWGDDPCAITRKPGVYTVCKYV 272
DB 181 NITDTMVCASVOEGGKDSQCGDSGGLVNCNLSQGIISWGDDPCAITRKPGVYTVCKYV 240
QY 273 DWIOETMKNN 282
DB 241 DWIOETMKNN 250

RESULT 13
US-10-141-702-506
Sequence 506, Application US/10141702
Publication No. US20030134358A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C208
CURRENT APPLICATION NUMBER: US/10/141,702
CURRENT FILING DATE: 2002-05-08
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
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;; SEQ ID NO 506
;; LENGTH: 250
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-141-702-506

Query Match 89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1,3e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 MRLIQLLLALATGTVGGETRIIKGFECCKPHSQPQOALFEKTRLLCGATLIAPRWLLTA 92
DB 1 MRLIQLLLALATGTVGGETRIIKGFECCKPHSQPQOALFEKTRLLCGATLIAPRWLLTA 60
QY 93 AHCLKPRYIVHLGQHNLOKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPV 152
DB 61 AHCLKPRYIVHLGQHNLOKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPV 120
QY 153 SITWAVRPLTSSRCVTAGTSCLSIGWGSTSSPOLRLPHTLRCAINTIIEHOKCENAYPG 212
DB 121 SITWAVRPLTSSRCVTAGTSCLSIGWGSTSSPOLRLPHTLRCAINTIIEHOKCENAYPG 180
QY 213 NITDTMVCASVOEGGKSCQDSCGPLYCNOSLOGIISWGDDPCAITRKPGVYTKVCXYV 272
DB 181 NITDTMVCASVOEGGKSCQDSCGPLYCNOSLOGIISWGDDPCAITRKPGVYTKVCXYV 240
QY 273 DWIOETMKNN 282
DB 241 DWIOETMKNN 250

RESULT 14
US-10-141-704-506
; Sequence 506, Application US/10141704
; Publication No. US20030134359A1

;; GENERAL INFORMATION:

;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Beresini, Maureen
;; APPLICANT: DeForge, Laura
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Sherwood, Steven
;; APPLICANT: Smith, Victoria
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tunas, Daniel
;; APPLICANT: Watanabe, Colin K
;; APPLICANT: Wood, William
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; FILE REFERENCE: P3330R1C209
;; CURRENT APPLICATION NUMBER: US/10/141,704
;; PRIOR FILING DATE: 2002-05-08
;; PRIOR APPLICATION REMOVED - See Palm or File Wrapper
;; NUMBER OF SEQ ID NOS: 550
;; SEQ ID NO 506
;; LENGTH: 250
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-141-704-506

Query Match 89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1,3e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 MRLIQLLLALATGTVGGETRIIKGFECCKPHSQPQOALFEKTRLLCGATLIAPRWLLTA 92
DB 1 MRLIQLLLALATGTVGGETRIIKGFECCKPHSQPQOALFEKTRLLCGATLIAPRWLLTA 60

QY 93 AHCLKPRYIVHLGQHNLOKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPV 152
DB 61 AHCLKPRYIVHLGQHNLOKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPV 120
QY 153 SITWAVRPLTSSRCVTAGTSCLSIGWGSTSSPOLRLPHTLRCAINTIIEHOKCENAYPG 212
DB 121 SITWAVRPLTSSRCVTAGTSCLSIGWGSTSSPOLRLPHTLRCAINTIIEHOKCENAYPG 180
QY 213 NITDTMVCASVOEGGKSCQDSCGPLYCNOSLOGIISWGDDPCAITRKPGVYTKVCXYV 272
DB 181 NITDTMVCASVOEGGKSCQDSCGPLYCNOSLOGIISWGDDPCAITRKPGVYTKVCXYV 240
QY 273 DWIOETMKNN 282
DB 241 DWIOETMKNN 250

RESULT 15
US-10-142-421-506
; Sequence 506, Application US/10142421
; Publication No. US20030134360A1

;; GENERAL INFORMATION:

;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Beresini, Maureen
;; APPLICANT: DeForge, Laura
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Sherwood, Steven
;; APPLICANT: Smith, Victoria
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tunas, Daniel
;; APPLICANT: Watanabe, Colin K
;; APPLICANT: Wood, William
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; FILE REFERENCE: P3330R1C218
;; CURRENT APPLICATION NUMBER: US/10/142,421
;; PRIOR FILING DATE: 2002-05-09
;; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
;; NUMBER OF SEQ ID NOS: 550
;; SEQ ID NO 506
;; LENGTH: 250
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-142-421-506

Query Match 89.0%; Score 1355; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1,3e-126;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 MRLIQLLLALATGTVGGETRIIKGFECCKPHSQPQOALFEKTRLLCGATLIAPRWLLTA 92
DB 1 MRLIQLLLALATGTVGGETRIIKGFECCKPHSQPQOALFEKTRLLCGATLIAPRWLLTA 60
QY 93 AHCLKPRYIVHLGQHNLOKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPV 152
DB 61 AHCLKPRYIVHLGQHNLOKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPV 120
QY 153 SITWAVRPLTSSRCVTAGTSCLSIGWGSTSSPOLRLPHTLRCAINTIIEHOKCENAYPG 212
DB 121 SITWAVRPLTSSRCVTAGTSCLSIGWGSTSSPOLRLPHTLRCAINTIIEHOKCENAYPG 180
QY 213 NITDTMVCASVOEGGKSCQDSCGPLYCNOSLOGIISWGDDPCAITRKPGVYTKVCXYV 272
DB 181 NITDTMVCASVOEGGKSCQDSCGPLYCNOSLOGIISWGDDPCAITRKPGVYTKVCXYV 240

Fri Oct 24 14:08:10 2003

us-09-856-320a-2.rapb

Page 9

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Db	241	DWIOETMKN	250

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Job time : 30.0411 secs

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6:	/SDSI1/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
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23:	/SDSI1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed

and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1523	100.0	1106	20	AAZ22638	CASB12 nucleotide derived from
2	1523	100.0	1158	20	AAZ22639	CASB12 derived from
3	1523	100.0	1186	24	ABK92131	Prostate cancer-associated
4	1523	100.0	1186	25	ABX76468	Lung cancer-associated
5	1523	100.0	1204	21	AAA317072	Human PBO1279 (UNC)
6	1523	100.0	1204	22	AAAS21496	Human CDNA sequence
7	1523	100.0	1204	22	AAAF54320	DNA encoding protein
8	1523	100.0	1204	22	ABL95664	Human angiotensin
9	1523	100.0	1204	24	ABL88175	Human PBO1279 CDNA
10	1523	100.0	1204	24	ABK33628	CDNA encoding human
11	1523	100.0	1204	25	ACA03855	CDNA encoding human
12	1523	100.0	1204	25	ACA04276	Human CDNA encoding
13	1523	100.0	1204	25	ABX98393	DNA encoding novel
14	1523	100.0	1301	21	AAAF1793	CDNA encoding human
15	1523	100.0	1314	21	AAZ330222	CDNA encoding a human
16	1519	99.7	1292	22	ABZ83372	Human secreted protein
17	1492.5	98.0	1335	22	ABZ46872	Nucleotide sequence
18	1410	92.6	1192	22	AAD14841	Human P513 gene C
19	1398	91.8	1166	22	AAD14841	Human P513 conserved
20	1388.5	91.2	934	21	AAAF1765	CDNA encoding human
21	1380	90.6	1191	20	AAAF9777	Extended human seed
22	1284	84.3	1146	20	AAV84589	Human secreted protein
23	1284	84.3	1146	22	AAV84589	Human secreted protein
24	1279.5	84.0	1164	24	ABSS1683	DNA encoding human
25	1233	81.0	833	19	AAV42925	DNA encoding a human
26	1227	80.6	1052	21	AAAC9798	Activation construct
27	1227	80.6	1052	22	AAAF5270	Nucleotide sequence
28	1187	77.9	1323	21	AAAF61764	CDNA encoding mouse
29	981	64.4	762	21	AAH31051	Human colon cancer
30	981	64.4	762	21	AAH31051	Human colon cancer
31	916.5	60.2	618	24	ABK30233	Human G-protein-coupled
32	769.5	50.5	1438	24	ABO98955	Human G-protein-coupled
33	758	49.8	1375	22	AAAS2876	Human coding sequence
34	754	49.5	1365	22	AAAS41087	Human CDNA encoding
35	739	48.5	472	24	ABK30366	CDNA encoding novel
36	736	48.3	924	22	AAAS41622	CDNA encoding novel
37	736	48.3	924	22	AAAS26948	Human CDNA encoding
38	736	48.3	924	23	ABK41855	CDNA encoding novel
39	698.5	45.9	1322	23	AB199534	Mouse ischaemic control
40	698.5	45.9	1333	17	AAT48519	Human neurotrophin gene
41	698.5	45.9	1333	18	AAT63251	Mouse neurotrophin gene
42	696	45.7	963	24	AAD30570	Human proteinase, PRP
43	696	45.7	963	24	ABK1774	DNA encoding novel
44	692.5	45.5	1278	24	ABK48347	CDNA encoding novel
45	690.5	45.3	1343	20	AAZ28633	Nucleotide sequence

ALIGNMENTS

RESULT 1	AAZ22638	AAZ22638 standard; CDNA, 1106 BP.
ID	AAZ22638	
XX	AAZ22638;	
XX		
AC	08-DEC-1999	(first entry)
DT		
XX		
DE	CASB12	nucleotide sequence.
XX		
XX	neurospisin; cancer; assay; inhibibility	
KW	ds.	
KM		
XX		
XX		
OS	Homo sapiens.	
XX		
XX		
PH	Key	Location/Qualifie
FT		14..862
TT	CDS	

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FT      /*tag= a
FT      /product= CASB12
XX      WO9949055-A1.
XX      30-SEP-1999.
XX      PD
XX      17-MAR-1999; 99WO-EP01894.
XX      PR
XX      20-MAR-1998; 98GB-0006095.
XX      (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX      PA
XX      PI Bruck CEM, Cassart J, Coche T, Vinals-Bassols C;
XX      DR WPI; 1999-580450/49.
XX      DR P-PSDB; AAY42439.
XX      PT New human serine protease CASB12, for treatment, prevention and
XX      diagnosis of cancer and autoimmune diseases
XX      PS Claim 10; Page 47; 58pp; English.
XX      CC This is the nucleotide sequence of the CASB12 gene. The nucleotide
XX      CC sequence of AA222638 shows homology with neuropilin and the encoded
XX      CC protein AA142439 is structurally related to other proteins of the
XX      CC serine protease family, having homology and/or structural similarity
XX      CC with neuropilin. It is expected that as well as similar structure, these
XX      CC proteins will also share similar biological functions and properties.
XX      CC The CASB12 polypeptides and polynucleotides can be used to develop
XX      CC methods for identifying agonists and antagonists/inhibitors of these
XX      CC molecules, and thereby treating conditions associated with CASB12
XX      CC polypeptide imbalance. The invention also provides for diagnostic assays
XX      CC for detecting diseases associated with inappropriate CASB12 polypeptide
XX      CC activity or levels.
XX      CC Since CASB12 is either specifically expressed or highly over-expressed
XX      CC in tumors compared to normal cells, the polypeptides and polynucleotides
XX      CC of the invention are believed to be important immunogens for specific
XX      CC prophylactic or therapeutic immunization against tumors. The
XX      CC polypeptides and polynucleotides can therefore be targeted by antigen
XX      CC specific immune reactions (which result in the destruction of the tumor
XX      CC cell) or they can be used to diagnose the occurrence of tumor cells.
XX      SQ Sequence 1106 BP, 247 A; 348 C; 287 G; 224 T; 0 other;

Alignment Scores:
Pred. No.: 2,24e-122 Length: 1106
Score: 1523.00 Matches: 282
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 20 Gaps: 0

US-09-856-320A-2 (1-282) x AA222638 (1-1106)
QY      1 MetGlnAqLeuAryTrpLeuAryAspTrpLysSerSerGlyAryGlyLeuThraAla 20
DB      14 ATGCAGAGGTTGAGGTGGCTGCGGAGCTGGAGATCATCGGAGAGGTCTCACAGACGC 73
QY      21 LysGluProGlyAlaArySerSerProLeuGlnAlaMetAryIleuGlnLeuIleu 40
DB      74 AAGGAACCTGGGGCCGCTCTCCCTCCAGGAGCATGAGGATTTCTGAGTTAACTCTG 133
QY      41 LeuAlaLeuAlaThrGlyLeuValGlyGlyGluThrAryIleIleLysGlyPheGluCys 60
DB      134 CTTCCTCTGGCAACAGGGCTTTAGGGGAGAGACAGATATCATAGGGCTTCAGAGTC 193
QY      61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGluLysThrAryLeuLeuCysGly 80
DB      194 AAGCTCACTCCACCCCTGGCAGCAGCCCTGTTGAGAAACACCCGGCTACTCTGTGGG 253
QY      81 AlaThrLeuIleAlaProAryTrpLeuLeuThraAlaHisCysLeuLysProAryTyr 100

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DB      254 GCGAGCTCATCGCCCGCCAGATGGCTCTGTACAGACGCCACTGCTCAACCGCCGTAC 313
QY      101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlyGlyGluGlnThrAryThr 120
DB      314 ATAGTTACACTGGGGAGACACACCTCCAGAAAGAGAGGGCTGTGAGACACCCGAGACA 373
QY      121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAsnHisArg 140
DB      374 GCCACTGAGTCTTCTCCCGCCAGCTTCTTCAACAACACCTTCCCAACAAAGACCACTGC 433
QY      141 AsnAspIleMetLeuValIleMetAlaSerProValSerIleThrTrpAlaValArgPro 160
DB      434 AATGACATCATCTCTGTGTAAGATGGCATGCCAGCTTCATCATCTGGCTGTGAGACC 493
QY      161 LeuThrLeuSerSerAryGlyValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
DB      494 CTCACCTCTCTCTCAGCTGTGTGCTGCTGACAGCTGCTGATTTCCGGCTGGGGGC 553
QY      181 SerThrSerSerProGlnLeuAryLeuProHisThrLeuAryGlyAlaAsnIleThrIle 200
DB      554 AGCAGTCTCACGCCCCAGATTACGCTGCTTACACCTTGCGATGCGCCAAACATCACCATC 613
QY      201 IleGluHisGlnLysCysGluAsnAlaTyrProGlyAsnIleThrAryThrMetValCys 220
DB      614 ATTGAGCACCGAAGTGTGAGAACGCTTACCCCGGCACATCATCACAGACCATGTGTGT 673
QY      221 AlaSerValGlnGluGlyLysAspSerCysGlnGlyAspSerGlyLysProLeuVal 240
DB      674 GCCAGCGTGAGAAAGGGGGCAAGAGACTCTGCCAGGGTGACTCCGGGGCCCTCTGTGTC 733
QY      241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
DB      734 TGTAAACGATGCTCTTCAAGGATTAATCTCTGGGGCCAGATCGGTGCGATACACCGGA 793
QY      261 LysProGlyValTyrThrLysValCysLeuIleValAspTrpIleGlnGluThrMetLys 280
DB      794 AAGCTGTGTCTTACAGAAAGTGTGCAAAATATGTGAGCTGATCCAGAGACCATGTAG 853
QY      281 AsnAsn 282
DB      854 AACCAAT 859

RESULT 2
AA222639
ID      AA222639 standard; cDNA; 1158 BP.
XX      AC
XX      AA222639;
XX      DT 08-DEC-1999 (first entry)
XX      DE CASB12 derived from Expressed Sequence Tag sequences.
XX      KW neuropilin; cancer; assay; inhibitor; serine protease; immunogenic;
XX      KW autoimmune disease; ds.
XX      OS Homo sapiens.
XX      FH
XX      Key Location/Qualifiers
XX      CDS 84..932
XX      FT /*tag= a
XX      FT /product= CASB12
XX      PA
XX      PI Bruck CEM, Cassart J, Coche T, Vinals-Bassols C;

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XX WPI: 1999-580450/49.
 DR P-PSDB: AAY42440.
 XX
 PT New human serine protease CASB12, for treatment, prevention and
 diagnosis of cancer and autoimmune diseases
 XX
 PS Claim 26; Page 49; 58pp; English.
 XX
 CC This is the nucleotide sequence of the CASB12 gene derived from
 CC Expressed Sequence Tag (EST) search for tumor-specific and
 CC tumor-associated antigens. The nucleotide sequence of AA222638 shows
 CC homology with neuropilin and the encoded protein AAY42439 is structurally
 CC related to other proteins of the serine protease family, having homology
 CC and/or structural similarity with neuropilin. It is expected that as well
 CC as similar structure, these proteins will also share similar biological
 CC functions and properties.
 CC The CASB12 polypeptides and polynucleotides can be used to develop
 CC methods for identifying agonists and antagonists/inhibitors of these
 CC molecules, and thereby treating conditions associated with CASB12
 CC polypeptide imbalance. The invention also provides for diagnostic assays
 CC for detecting diseases associated with inappropriate CASB12 polypeptide
 CC activity or levels.
 CC Since CASB12 is either specifically expressed or highly over-expressed
 CC in tumors compared to normal cells, the polypeptides and polynucleotides
 CC of the invention are believed to be important immunogens for specific
 CC prophylactic or therapeutic immunization against tumors. The
 CC polypeptides and polynucleotides can therefore be targeted by antigen
 CC specific immune reactions (which result in the destruction of the tumor
 CC cell) or they can be used to diagnose the occurrence of tumor cells
 SQ Sequence 1158 BP; 274 A; 359 C; 306 G; 219 T; 0 other;

Alignment Scores:
 Pred. No.: 2,38e-122 Length: 1158
 Score: 1523.00 Matches: 282
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0

US-09-856-320A-2 (1-282) x AA222639 (1-1158)

QY 1 MetGlnArgLeuAyrGTrpLeuArgAspTrpLysSerSerGlyAryGlyLeuThrAlaAla 20
 DB ATGCAAGAGTTAGAGTGGCTGGGAGCTGAAAGTATCGGAGAGAGTTCCACAGAGCC 143
 QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleu 40
 DB AAGGAACCTGGGGCCCGCTCTCCCTCCAGGCCATAGAGATTCTGCAGTTATCTCG 203
 QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyLeuThrArgIleIleLysGlyPheGlyCys 60
 DB CTTCGCTCTGGCAACAGGGCTTGTAGGGGAGAGACAGCATATCATAGGGGTTCCAGATCC 263
 QY 61 LysProHisSerSerGlyProTrpGlnAlaAlaPheGlyLeuThrArgLeuLeuGly 80
 DB AAGCTCTACTCCCAAGCCCTGGAGAGGAGGCTGTGGAAGAAGCGGCTACTCTGTGGG 323
 QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTrp 100
 DB GGAGCGCTCATGCCGCCGAGATGGCTCTGACAGAGCCCACTGCTCAAGCCCGCTAC 383
 QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlyGlyGlyGlyGlnThrArgThr 120
 DB ATAGTTTCACTGGGAGAGCAACCTCCAGAGGAGGGCTGTGAGAGAGACCCGGACA 443
 QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
 DB GGCACTGAGCTCTTCCCAACCCCGGCTTCAACACAGGCTCCCAACCAACCAACCGC 503
 QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160

DB 504 AATGACATCATCTGCTGATGAGATGCATGCCAGTCTCCATCATCCTGGGCTGCGACCC 563
 QY 161 LeuThrLysSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
 DB CTCACCTCTCTCTCAAGCTGTCTACTGCTGGACACAGCTGCTCATTTCCGGCTGGGCG 623
 QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
 DB AGCAGCTCCAGCCGCCAGTTAGCTGCTGCTCACCCTTCGATCGCCCAACATCACCATC 683
 QY 201 IleGluHisLeuLysCysGluAsnAlaTrpProGlyAsnIleThrAspThrMetValCys 220
 DB ATTGACACACCAAGAGTGTAGAACCTCTACCCCGCAATCATCAGACACCATGGTGT 743
 QY 221 AlaSerValGlnGlnGlyGlyLysAspSerCysGlnGlyAspSerGlyGlyProLeuVal 240
 DB GCCACGTCAGAGGAAGGGGCAAGACTCTCCAGGGGAGTCTCCGGGGCCCTCTGGTTC 803
 QY 241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
 DB TGTAACTAGTCTCTTCAAGGCTTATCTCTGGGGCCAGATCCGTTCGATCACCCGA 863
 QY 261 LysProGlyValTrpThrLysValCysLysTrpValAspTrpIleGlnIleThrMetLys 280
 DB AAGCTGTGTGTCTACACCAAGTGTGCAAAATATGTGACTGTGATTCAGAGACGATGAAG 923
 QY 281 AsnAsn 282
 DB 924 AACCAAT 929

RESULT 3

ID ABR92131 standard; DNA; 1186 BP.

AC ABR92131;

DT 15-AUG-2002 (first entry)

DE Prostate cancer-associated DNA sequence #17.

KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;

KW gene therapy; gene; ds.

OS Mammalia.

PN WO200230268-A2.

PD 18-APR-2002.

PF 12-OCT-2001; 2001WO-US32045.

PR 13-OCT-2000; 2000US-0687576.

PR 08-DEC-2000; 2000US-0733288.

PR 08-DEC-2000; 2000US-0733742.

PR 24-JAN-2001; 2001US-263957P.

PR 16-MAR-2001; 2001US-276791P.

PR 06-APR-2001; 2001US-286212P.

PR 24-APR-2001; 2001US-0847046.

PR 04-MAY-2001; 2001US-288589P.

PA (EOSB-) EOS BIOTECHNOLOGY INC.

XX Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;

DR WPI: 2002-471335/50.

XX P-PSDB: ABR61816.

PT Detecting a prostate cancer-associated transcript in a cell in a

PT patient, useful for diagnosing prostate cancer (PC) or screening

PT modulators of PC, by determining if prostate cancer-associated genes

are expressed in a prostate tissue

XX Claim 22; Page 313; 436bp; English.
PS
XX The present invention relates to methods of detecting a prostate
CC cancer-associated transcript in a cell from a patient. The method
XX comprises contacting a biological sample from the patient with
CC prostate cancer-associated polynucleotides (designated PC genes) that
CC selectively hybridize to a sequence that is at least 80% identical
CC to them. The prostate cancer-associated polynucleotide sequences
CC are differentially expressed in prostate tumor tissue or in
CC prostate cancer and are derived from the tissues of various
CC organisms such as humans or other mammals (e.g. mice, sheep and dogs).
CC The methods of the invention are useful for diagnosing and treating
CC prostate cancer in mammals. The prostate cancer-associated genes are
CC useful for diagnosing or treating prostate cancer, as well as for
CC identifying modulators of prostate cancer or agents that inhibit
CC prostate cancer. The nucleic acid sequences are particularly useful
CC in gene therapy, as a vaccine or in antisense applications.
CC ABK2115-ABK92263 represent prostate cancer-associated polynucleotide
CC sequences.
XX
SQ Sequence 1186 BP; 272 A; 368 C; 302 G; 244 T; 0 other;

Alignment Scores:

Pred. No.: 2,45e-122 Length: 1186
Score: 1523.00 Matches: 282
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0

US-09-856-320A-2 (1-282) x ABK92131 (1-1186)

QY 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaAla 20
DB 26 ATGCAGAGGTTAGAGCGCTGCGGAGACTGGAAGTATATCCGCGAGCTTCACAGCC 85
QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeu 40
DB 86 AAGGAACCTGGGGCGCTCTCCCTCCAGCCATAGAGATTCTGCAGTTAATCTCG 145
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyIleuTrpArgIleIleuGlyIleuGly 60
DB 146 CTGGCTCTGGCAACAGGCTTGTAGGGGAGAGACCAGGATATCAAGGGGTTCAAGTCC 205
QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGluLysThrArgLeuGly 80
DB 206 AAGCTCACTCCAGGCTGCGAGGAGGCTGTTGANAAGACGGGCTACTGTGGG 265
QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
DB 266 GCGAGCGCTATGCCCCGATGGCTCTGACAGAGCCCACTGGCTCAAGCCCGCTAC 325
QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlyCysGlnGlnThrArgThr 120
DB 326 ATAGTTCACTGGGAGACCAACCTCCGAAGAGAGAGGCTGTGAGCAGACCGGACA 385
QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
DB 386 GGCACGTGACTCTTCCCAACCCCGGCTTCACAAACAGCTCCCAACAACAACACCCG 445
QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
DB 446 AATGACATCATGCTGTGTAAGATGGATGGCAGTCTCATCACTGGGCTGTGAGACC 505
QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
DB 506 CTCACCTCTCTCTCAGCTGTCTACTGTGACACCAAGTGTCTAATTTCCGGCTGGGG 565
QY 181 SerTrpSerSerProGlnLeuArgLeuProHisTrpLeuArgCysAlaAsnIleThrIle 200
DB 566 AGCAGCTCAAGCCCAAGTTAGCGCTGCTCAACACTTGGCGATGGCCCAACATCACCATC 625

QY 201 IleGluHisGlnLysCysGlnAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220
DB 626 ATTGAGCCACCAAGTGTGAGAAAGCCCTACCCCGGCAACATCAAGACCATGCTGTGT 685
QY 221 AlaSerValGlnGluGlyGlyLysAspSerCysGlnGlyAspSerGlyGlyProLeuVal 240
DB 686 GCGACGCTGCGAGAAAGGGGCAAGGACTCTCCGAGGCTGACTCGGGGCGCTCTGTGTC 745
QY 241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
DB 746 TGTAACCACTCTCTTCAAGGATTAATCTCTGGGGCCAGATCCGTGTGCATCACCCGA 805
QY 261 LysProGlyValTyrThrLysValCysLysTrpValAspTrpIleGlnGluThrMetLys 280
DB 806 AAGCTGTGTCTACACCAAGTCTGCAAAATATGTGACTGATTCAGAGACCATGAAG 865
QY 281 AsnAsn 282
DB 866 AACCAAT 871

RESULT 4

ID ABX76468 standard; DNA; 1186 BP.

AC ABX76468;

DT 02-APR-2003 (first entry)

DE Lung cancer-associated polynucleotide #32.

KW Lung cancer-associated polynucleotide; gene; ds; cytosolic; emphysema;
KW antiinflammatory; antisthmatic; non-small cell lung cancer; atelectasis;
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

OS Unidentified.

PN WO200286443-A2.

PD 31-OCT-2002.

PP 18-APR-2002; 2002WO-US12476.

PR 18-APR-2001; 2001US-284770P.

PR 10-MAY-2001; 2001US-290492P.

PR 09-NOV-2001; 2001US-339245P.

PR 13-NOV-2001; 2001US-350666P.

PR 29-NOV-2001; 2001US-334370P.

PR 12-APR-2002; 2002US-372246P.

PA (EOSB-) EOS BIOTECHNOLOGY INC.

PI Aziz N. Murray R;

DR WPI; 2003-093161/08.

DR P-PSDB; ABUS6739.

PT Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer.

PS Claim 22; Page 443; 453bp; English.

XX The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridises
CC to a sequence that is at least 80% identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung
CC cancer-associated polynucleotides and polypeptides are used for
CC identifying a compound that modulates a lung cancer-associated
CC polypeptide, for inhibiting proliferation of a lung cancer-associated


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PR 23-SEP-1998; 98US-0101472.
PR 23-SEP-1998; 98US-0101474.
PR 23-SEP-1998; 98US-0101475.
PR 23-SEP-1998; 98US-0101476.
PR 23-SEP-1998; 98US-0101477.
PR 23-SEP-1998; 98US-0101479.
PR 24-SEP-1998; 98US-0101738.
PR 24-SEP-1998; 98US-0101738.
PR 24-SEP-1998; 98US-0101741.
PR 24-SEP-1998; 98US-0101743.
PR 24-SEP-1998; 98US-0101915.
PR 24-SEP-1998; 98US-0101916.
PR 29-SEP-1998; 98US-0102207.
PR 29-SEP-1998; 98US-0102240.
PR 29-SEP-1998; 98US-0102307.
PR 29-SEP-1998; 98US-0102310.
PR 29-SEP-1998; 98US-0102331.
PR 30-SEP-1998; 98US-0102484.
PR 30-SEP-1998; 98US-0102487.
PR 30-SEP-1998; 98US-0102570.
PR 30-SEP-1998; 98US-0102571.
PR 01-OCT-1998; 98US-0102684.
PR 01-OCT-1998; 98US-0102687.
PR 02-OCT-1998; 98US-0102687.
PR 06-OCT-1998; 98US-0103258.
PR 06-OCT-1998; 98US-0103449.
PR 07-OCT-1998; 98US-0103314.
PR 07-OCT-1998; 98US-0103315.
PR 07-OCT-1998; 98US-0103328.
PR 07-OCT-1998; 98US-0103395.
PR 07-OCT-1998; 98US-0103396.
PR 07-OCT-1998; 98US-0103401.
PR 08-OCT-1998; 98US-0103633.
PR 08-OCT-1998; 98US-0103678.
PR 08-OCT-1998; 98US-0103679.
PR 08-OCT-1998; 98US-0103711.
PR 14-OCT-1998; 98US-0104257.
PR 20-OCT-1998; 98US-0104987.
PR 20-OCT-1998; 98US-0105000.
PR 20-OCT-1998; 98US-0105002.
PR 21-OCT-1998; 98US-0105104.
PR 22-OCT-1998; 98US-0105169.
PR 22-OCT-1998; 98US-0105266.
PR 26-OCT-1998; 98US-0105693.
PR 26-OCT-1998; 98US-0105694.
PR 27-OCT-1998; 98US-0105807.
PR 27-OCT-1998; 98US-0105881.
PR 27-OCT-1998; 98US-0105882.
PR 27-OCT-1998; 98US-0106062.
PR 28-OCT-1998; 98US-0106023.
PR 28-OCT-1998; 98US-0106029.
PR 28-OCT-1998; 98US-0106030.
PR 28-OCT-1998; 98US-0106032.
PR 28-OCT-1998; 98US-0106033.
PR 28-OCT-1998; 98US-0106178.
PR 29-OCT-1998; 98US-0106248.
PR 29-OCT-1998; 98US-0106384.
PR 29-OCT-1998; 98US-0106500.
PR 30-OCT-1998; 98US-0106464.
PR 03-NOV-1998; 98US-0106856.
PR 03-NOV-1998; 98US-0106902.
PR 03-NOV-1998; 98US-0106905.
PR 03-NOV-1998; 98US-0106919.
PR 03-NOV-1998; 98US-0106932.
PR 03-NOV-1998; 98US-0106934.
PR 10-NOV-1998; 98US-0107783.
PR 17-NOV-1998; 98US-0108775.
PR 17-NOV-1998; 98US-0108779.
PR 17-NOV-1998; 98US-0108787.
PR 17-NOV-1998; 98US-0108788.
PR 17-NOV-1998; 98US-0108801.
PR 17-NOV-1998; 98US-0108802.
PR 17-NOV-1998; 98US-0108806.
PR 17-NOV-1998; 98US-0108807.

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PR 17-NOV-1998; 98US-0108867.
PR 17-NOV-1998; 98US-0108925.
PR 18-NOV-1998; 98US-0108848.
PR 18-NOV-1998; 98US-0108849.
PR 18-NOV-1998; 98US-0108849.
PR 18-NOV-1998; 98US-0108850.
PR 18-NOV-1998; 98US-0108851.
PR 18-NOV-1998; 98US-0108852.
PR 18-NOV-1998; 98US-0108858.
PR 18-NOV-1998; 98US-0108904.
PR (GETH ) GENENTECH INC.
PA
XX
XX Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
XX WPI, 2000-237871/20.
XX P-PSDB; AAY99390.
DR
PT New mammalian DNA sequences encoding transmembrane, receptor or
PT secreted PRO polypeptides, useful for screening of potential peptide or
PT small molecule inhibitors of the relevant receptor/ligand interactions
XX
XX Claim 2, Fig 101, 773pp; English.
XX
XX AAA37022 to AAA37144 encode the new isolated human transmembrane,
CC receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
CC transmembrane and receptor PRO proteins can be used for screening of
CC potential peptide or small molecule inhibitors of the relevant
CC receptor/ligand interactions. The polypeptides and nucleotide sequences
CC encoding then have various industrial applications, including uses as
CC pharmaceutical and diagnostic agents. AAA37145 to AAA37310 represent
CC PCR primers and hybridisation probes used in the isolation of the PRO
CC polypeptides from the present invention.
XX
SQ Sequence 1204 BP, 306 A, 364 C, 294 G, 240 T, 0 other;

Alignment Scores:
Prism. No.: 2,5e-122 Length: 1204
Score: 1523.00 Matches: 282
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-856-320A-2 (1-282) x AAA37072 (1-1204)
QY 1 MetGlnArgLeuAaGTrpLeuAaGAspTrpLysSerSergIyArgGlyLeuThrAla 20
DB 10 ATGCAAGAGCTTGAGGTGCTGCGGAGCTGAAGTCATCGGCGAGGCTTCACAGCACC 69
QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeu 40
DB 70 AAGGAACCTGGGGCCGCTCTCCCTCCAGGCCCAAGAGATTCGACGTTAATCTTG 129
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyGlnThrArgIleIleGlyPheGluCys 60
DB 130 CTGCTCGGCAACAGGCTTGTAGGGGAGAGACAGACATCAACGGGTTCCAGTCC 189
QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGluIlyThrArgLeuLysGly 80
DB 190 AAGCTCACTCCAGCCCTGCGAGGACGCTGTTCGAGAGAGCGCGCTACTCTGTGG 249
QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaHisCysLeuLysProArgTyr 100
DB 250 GCGAGGCTCATCGGCCCCAGATGCTCTGCACACAGCCCTCCTCAAGCCCCGGCTAC 309
QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGluGluGlyCysGluGlnThrArgThr 120
DB 310 ATAAGTTCACCTGGGGCAGACAACTCCAGAGAGAGAGAGGCTGTGACCAACCCGGACA 369
QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
DB 370 GCCACTGAGTCTTCCCCCAAGGCTTCAACAAGAGCTTCCCAAGAGACACCGCC 429

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QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
 DB 430 ATGACATCATGCTGCTGAAGATGGCATGCCACGCTCCATCATCTGGGCTGTGCACCC 489
 QY 161 LeuThrLeuSerSerArgCysValIThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
 DB 490 CTCACCTCTCTCCACGCTGTGTCACTGCTGGACACAGCTGCTCATTTCCGGCTGGGC 549
 QY 181 SerThrSerSerProGlnLeuValGluLeuProIleThrLeuArgCysAlaAsnIleThrIle 200
 DB 550 AGCAGCTCCAGCCCCCAGTTACGCTGCTCCACACCTTGCGAGTCCGCCAATCATCACCATC 609
 QY 201 IleGlnHisGlnLysCysGluAsnAlaIleProGlyAsnIleThrAspThrMetValCys 220
 DB 610 ATTGACACACAGAAAGTGTGAACGCTACCCCGGCAACATCATACAGACCAATGAGTGT 669
 QY 221 AlaSerValGlnGluGlyValLysAspSerCysGlnGlyAspSerGlyValProLeuVal 240
 DB 670 GCCAGGCTCAGAGAGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 729
 QY 241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
 DB 730 GTTAACTAGTCTCTTCAAGGCAATTATCTCTGAGGAGAGAGAGAGAGAGAGAGAGAG 789
 QY 261 LysProGlyValIleThrLysValCysLysIleValAspTrpIleGlnIleThrMetLys 280
 DB 790 AAGCTGTGTCTCAACGAAAGCTCTCAATATATGTGATCGATCCAGAGAGAGAGAGAG 849
 QY 281 AsnAsn 282
 DB 850 AACCAAT 855

RESULT 6

AAS21496 standard; cDNA; 1204 BP.

ID AAS21496 standard; cDNA; 1204 BP.
 AC AAS21496;
 DT 24-OCT-2001 (first entry)
 DE Human cDNA sequence encoding for PRO1279 polypeptide.
 XX
 KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;
 KW breast; prostate; cervical; tumour necrosis factor- α ; TNF- α ;
 KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
 KW adipocyte; A-peptide; factor VIIA; gene therapy; ss.
 XX
 OS Homo sapiens.
 OS
 PN WO200140466-A2.
 PD 07-JUN-2001.
 XX
 PF 01-DEC-2000; 2000WO-US32678.
 XX
 PR 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28564.
 PR 09-DEC-1999; 99US-0170262.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 20-DEC-1999; 99WO-US30999.
 PR 30-DEC-1999; 99WO-US31243.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.

PR 01-MAR-2000; 2000WO-US05601.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 10-NOV-2000; 2000WO-US30873.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W,
 PI Gertsen ME, Goddard A, Godowski RJ, Gunney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z,
 XX
 DR WPI; 2001-408281/43.
 DR P-PSDB; AAU12424.
 XX

PT Isolated, secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
 PT lung, breast, prostate, cervical
 XX
 PS Claim 3; Fig 505; 813pp; English.
 XX

CC AAS21244-AAS21518 encode for novel human secretory and transmembrane
 CC PRO polypeptides. The PRO polypeptides are useful to detect other
 CC PRO polypeptides, to link bioactive molecules to cells expressing
 CC PRO polypeptides, to modulate biological activities of cells expressing
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample.
 CC Some of the 275 sequences are also useful to stimulate the release of
 CC tumour necrosis factor- α (TNF- α) from human blood; the
 CC gene expression or differentiation of chondrocytes; the proliferation or
 CC gene expression in pericyte cells; the release of proteoglycans from
 CC cartilage; the proliferation of inner ear utricular supporting cells or
 CC of T-lymphocytes; the release of a cytokine from peripheral blood
 CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
 CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
 CC to factor VIIA. The PRO polypeptides can be used in assays to identify
 CC molecules involved in binding interactions. The polynucleotides encoding
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy.
 XX

SQ Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;

Alignment Scores:

Pred. No.:	2,56-122	Length:	1204
Score:	1523.00	Matches:	282
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	100.00%	Gaps:	0

US-09-856-320A-2 (1-282) x AAS21496 (1-1204)

QY 1 MetGlnArgLeuArgTrpLeuValGAspTrpLysSerSerGlyValThrAlaIle 20
 DB 10 ATGCAAGAGTTCAGTGGCTGCGGAGCTGGAAGTATATGGGACAGAGTCTCACAGACC 69
 QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleu 40
 DB 70 AAGGAACCTGGGGCCGCTCTCCCTCCAGGCAATGAGATTCGAGTTATCTCTG 129
 QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60
 DB 130 CTGCTCTGGCAACGAGGCTGTAGGGGAGAGACAGAGATATCAAGGGGTTCAAGTGC 189
 QY 61 LysProHisSerGlnProTrpGlnAlaIleuPheGluLysThrArgLeuLeuCysGly 80

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Db      190 AAGCTCACTCCAGCCCTGGAGGAGCCCTGTTGAGAGAACGGGCTACTCTGTGGG 249
QY      81 AATATTTTLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
Db      250 GGGAGCGCTCATGCCCCCGAGATGGCTCCGACAGACAGCCACTGCTCAAGCCCGCTAC 309
QY      101 ILeValHisLeuGlyGlnHisAsnLeuGlnLysGlnGlyCysGlnGlnThrArgThr 120
Db      310 ATAGTTTACCTGGGGGAGCACAACCTCCAGAGAGAGAGGGCTGTGAGCAGACCCGGACA 369
QY      121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
Db      370 GCCACTGAGTCTTCCCCCACCCTTCAACAACAGCTCCCAACAAGAACACACCGCC 429
QY      141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrAlaValArgPro 160
Db      430 AATGACATCATCTGGTGAAGATGGCATGCGACAGTCTCCATCACCCTGGGCTGTGACCC 489
QY      161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
Db      490 CTCACCTCTCTCTCAGCTGTGTCTACTGCTGGACACCGCTGCTCATTTCCGGCTGGGGC 549
QY      181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
Db      550 AGCAGCTCCAGCCCGCCAGTTAGCCTGCTCAGCTTGCATGCGCCAACTCACCATC 609
QY      201 ILeGluHisGlnLysCysGlnAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220
Db      610 ATTTGAGACACCAAGAGTGAAGAACGCTTACCCCGGCAACATCACAGACACCATGGTGT 669
QY      221 AlaSerValGlnGlnGlyLysAspSerCysGlnGlyAspSerGlyLysProLeuVal 240
Db      670 GCCACGCTGCAGAGAGGGGCAAGAGCTCTCTCCAGGGAGACTCCGGGGCCCTTGTGGTC 729
QY      241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
Db      730 TGTAACTGCTCTTCAAGGCATTTATCTCTCTGGGGCAGAGATCCGTTGCCATCACCCGA 789
QY      261 LysProGlyValTyrThrLysValCysLysTyrValAspTrpIleGlnGlnThrMetLys 280
Db      790 AAGCTGTGTCTACAGCAAGACTGTGCAAAATATGTGACTGATCAGAGACGATGTAAG 849
QY      281 AsnAsn 282
Db      850 AACCAAT 855

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RESULT 7

AAFs4320
ID AAFs4320 standard; DNA; 1204 BP.

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XX      AC      AAFs4320;
XX      DT      02-APR-2001 (first entry)
XX      DE      DNA encoding protein of the invention #51.
XX      KM      Secreted; transmembrane; gene therapy; ss.
XX      OS      Unidentified.
XX      PN      WO200078961-A1.
XX      PD      28-DEC-2000.
XX      PF      18-FEB-2000; 2000WO-US04342.
XX      PR      23-JUN-1999; 99US-0141037.
XX      PR      20-JUL-1999; 99US-0144758.
XX      PR      26-JUL-1999; 99US-0145698.
XX      PR      01-SEP-1999; 99WO-US20111.
XX      PR      29-OCT-1999; 99US-0162506.
XX      PR      30-NOV-1999; 99WO-US28313.
XX      PR      02-DEC-1999; 99WO-US28551.

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PR      16-DEC-1999; 99WO-US30095.
PR      05-JAN-2000; 2000WO-US00219.
PR      06-JAN-2000; 2000WO-US00376.
XX      XX      (GENTH ) GENENTECH INC.
PI      Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI      Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI      Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D;
PI      Watanabe CK, Williams PM, Wood WI;
DR      WPI; 2001-071395/08.
PT      Secreted and transmembrane proteins and nucleic acids designated PRO,
PT      useful as hybridization probes, in chromosome and gene mapping and gene
PT      therapy -
PS      Claim 2; Fig 101; 787pp; English.
CC      The present invention relates to secreted and transmembrane proteins.
CC      These proteins and the DNA encoding them may be used as hybridization
CC      probes, in chromosome and gene mapping and in the generation of
CC      anti-sense RNA and DNA. They may also be used used to generate either
CC      transgenic animals or knockout animals which are in turn useful for
CC      development and screening of therapeutically useful reagents.
CC      The nucleic acids may also be used in gene therapy.
SQ      Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;

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Alignment Scores:

Pred. No.:	25e-122	Length:	1204
Score:	1523.00	Matches:	282
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0

US-09-856-320A-2 (1-282) x AAFs4320 (1-1204)

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QY      1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAla 20
Db      10 ATGCAGAGGTTGAGGTGGCTCGGGAGCTGGAAGTCATCGGGCAGAGGCTCACAGCAGCC 69
QY      21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleLeu 40
Db      70 AAGAACTGGGGCCGCTCTCTCCCTCCAGGCCATGAGGATTCGCACTTAATCTTG 129
QY      41 LeuAlaLeuAlaThrGlyLeuValGlyGlyLysThrArgIleIleLysGlyPheGluCys 60
Db      130 CTGCTCTGGCACAAGGGCTTGTAGGGGAGAGACCGAGATCATCAAGGGTTGAGTGC 189
QY      61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGluLysThrArgLeuLeuCysGly 80
Db      190 AAGCTCACTCCAGCCCTGGCAGCAGCCCTGTTCGAGAAAGAGCGGCTACTCTGTGGG 249
QY      81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
Db      250 GCGAGCTCATGCGCCCGCCAGATGCTCTCTGACACAGCCCACTCTCAACCCCGCTAC 309
QY      101 ILeValHisLeuGlyGlnHisAsnLeuGlnLysGlnGlyCysGlnGlnThrArgThr 120
Db      310 ATAGTTTACCTGGGGGAGCACAACCTCCAGAGAGAGAGGGCTGTGAGCAGACCCGGACA 369
QY      121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
Db      370 GCCACTGAGTCTTCCCCCACCCTTCAACAACAGCTCCCAACAAGAACACACCGCC 429
QY      141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrAlaValArgPro 160
Db      430 AATGACATCATCTGGTGAAGATGGCATGCGACAGTCTCCATCACCCTGGGCTGTGACCC 489
QY      161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180

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Db      490 CTCACCTCTCTCAGCTGTGTACTGTCTGACCAAGCTGCTCATTTCCGGCTGGGC 549
Qy      181 SerThSerSerProGlnLeuAArgLeuProHleThLeuArgCysAlaSerHleThrile 200
Db      550 AGACCTCCAGCCCCCAAGTTACCCCTGCTCCACACCTTGGATGCGGCAACATCACCATC 609
Qy      201 HleGlnHleGlnLysCysGlnAanaIATyProGlyAsnHleThrAspThrMetValCys 220
Db      610 ATTGACACACAGAGTGTGAGAACGCTTACCCCGGCAACATCAGACACCATGCTGTGT 669
Qy      221 AlaSerValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 240
Db      670 GCCAGGCTGTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 729
Qy      241 CysAsnGlnSerLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 260
Db      730 TGTACACAGTCTCTTCAAGGCAATTATCTCTGGGGCCAGGATCCGTGTGATCACCAG 789
Qy      261 LysProGlyValTyThrLysValCysGlyTyValAspTyrIleGlnGlnThrMetLys 280
Db      790 AAGCCTGTGTCTACACGAAAGCTGCAATATATGTGAGATCGATCCAGGAGACGATGAG 849
Qy      281 Aaaaan 282
Db      850 AACCAAT 855

RESULT 8
ABL95664
ID      ABL95664 standard; cDNA, 1204 BP.
XX      ABL95664;
XX      19-JUL-2002 (first entry)
DE      Human angiogenesis related cDNA PRO1279 SEQ ID NO: 207.
XX      Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW      atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KM      cardiac; cytosolic; antiangiogenic; hypotensive; vulnery;
XX      antiarteriosclerotic; gene; ss.
XX      Homo sapiens.
XX      WO200208284-A2.
XX      31-JAN-2002.
XX      09-JUL-2001; 2001WO-US21735.
XX      20-JUL-2000; 2000US-219556P.
XX      25-JUL-2000; 2000US-220624P.
XX      28-JUL-2000; 2000US-220644P.
XX      02-AUG-2000; 2000US-222691P.
XX      17-AUG-2000; 2000US-0643657.
XX      23-AUG-2000; 2000WO-US23522.
XX      24-AUG-2000; 2000WO-US23328.
XX      07-SEP-2000; 2000US-230978P.
XX      15-SEP-2000; 2000US-000000P.
XX      18-SEP-2000; 2000US-0664610.
XX      18-SEP-2000; 2000US-0665350.
XX      24-OCT-2000; 2000US-242922P.
XX      08-NOV-2000; 2000US-0709238.
XX      08-NOV-2000; 2000WO-US30952.
XX      10-NOV-2000; 2000WO-US30873.
XX      01-DEC-2000; 2000WO-US32678.
XX      20-DEC-2000; 2000US-0747259.
XX      22-DEC-2000; 2000WO-US34956.
XX      22-JAN-2001; 2001US-0767609.
XX      28-FEB-2001; 2001US-0796498.
XX      28-FEB-2001; 2001WO-US06520.
XX      01-MAR-2001; 2001WO-US06666.
XX      09-MAR-2001; 2001US-0802706.

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PR      14-MAR-2001; 2001US-0808689.
PR      22-MAR-2001; 2001US-0816744.
PR      05-APR-2001; 2001US-0828366.
PR      10-MAY-2001; 2001US-0854208.
PR      10-MAY-2001; 2001US-0854280.
PR      25-MAY-2001; 2001US-0866028.
PR      25-MAY-2001; 2001US-0866034.
PR      25-MAY-2001; 2001WO-US17092.
PR      30-MAY-2001; 2001US-0870574.
PR      30-MAY-2001; 2001WO-US17443.
PR      01-JUN-2001; 2001WO-US17800.
PR      20-JUN-2001; 2001WO-US19692.
PR      28-JUN-2001; 2001WO-US00000.
XX      (GETH ) GENENTECH INC.
PA      (BAKE/) BAKER K P.
PA      (FERR/) FERRARA N.
PA      (GERB/) GERBER H.
PA      (GERR/) GERRITSEN M E.
PA      (GODD/) GODDARD A.
PA      (GODO/) GODOWSKI P J.
PA      (GURN/) GURNEY A L.
PA      (HILL/) HILLAN K J.
PA      (MARS/) MARSTERS S A.
PA      (PANJ/) PAN J.
PA      (PAON/) PAONI N F.
PA      (STEP/) STEPHAN J F.
PA      (WATA/) WATANABE C K.
PA      (WILL/) WILLIAMS P W.
PA      (WOOD/) WOOD W I.
XX      Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
PI      Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
PI      Stephan JF, Watanabe CK, Williams PW, Wood WI, Ye W;
DR      WPI; 2002-171999/22.
DR      P-PSDB; ABB95526.
XX      One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT      useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT      infarction), endothelial or angiogenic disorders in a mammal -
XX      Claim 1, Fig 207; 567pp; English.
XX      The present invention provides the protein and coding sequences of human
CC      PRO proteins. These are useful for treating or diagnosing a
CC      cardiovascular, endothelial or angiogenic disorder, including cardiac
CC      hypertrophy, trauma, cancer, age-related macular degeneration,
CC      atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC      angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC      angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC      healing. The present sequence is a coding sequence of the invention.
XX      SQ
XX      Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;
XX      Alignment Scores:
XX      Pred. No.: 2,5e-122 Length: 1204
XX      Score: 1523.00 Matches: 282
XX      Percent Similarity: 100.00% Conservative: 0
XX      Best Local Similarity: 100.00% Mismatches: 0
XX      Query Match: 100.00% Indels: 0
XX      DB: 24 Gaps: 0
XX      US-09-856-320A-2 (1-282) x ABL95664 (1-1204)
Qy      1 MetGlnArgLeuArgTyrLysSerSerGlyArgGlyLeuThrAla 20
Db      10 ATGCAGAGGTGAGGTGCTGCGGAGCTGGAAGTATGCGGAGAGGCTACACACACC 69
Qy      21 LysGlnProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeu 40
Db      70 AAGGAACCTGGGGCCGCTCTCCCTCCAGGAGGATTCAGATTATCTCTG 129

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QY 41 LeuAlaLeuAlaThGlyLeuValGlyGlyGluThrArgIleIleGlyGlyPheGlyCys 60
 DB 130 CTGGCTCTGGCAACAGGCGCTTGTAGGGGAGAGACAGATATATCAAGGGGTTCCAGTGC 189
 QY 61 LysProHisSerGlnProTrrpGlnAlaAlaPheGlnLysThrArgLeuLeuGlyGly 80
 DB 190 AAGCTCATCTCCAGCGCTGGCAGGCGAGCGCTTCTGAGAAACCGCGCTACTCTGTGGG 249
 QY 81 AlaThrLeuIleAlaProArgTrrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
 DB 250 GCGAGCTCATCGCCCGCCAGATGGCTCCCTGACAGAGCCCACTGCTCAAGCGCCGCTAC 309
 QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlyGluGlyCysGlnGlnThrArgThr 120
 DB 310 ATAGTTTCACTGGGGGAGCACAACCTCCAGAAAGAGAGGGGCTGTAGAGAGACCCGGAGA 369
 QY 121 AlaThrGlySerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
 DB 370 GCCACTGAGCTCTTCCCGCCAGCCCGGCTTCAACACAGCTCCCAACAAACACACCGC 429
 QY 141 AsnAspIleMetLeuValIysMetAlaSerProValSerIleThrTrrpAlaValArgPro 160
 DB 430 AATGACATCATCTGCTGTGAAGATGGATCGCAGTCTCCATCATCCTGGGCTGTGACGCC 489
 QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrrpGly 180
 DB 490 CTCACCTCTCTCCAGCTGTGTCACTGTGACACACAGCTGCTCATTTCCCGCTGGGGGC 549
 QY 181 SerThrSerSerProGlnLeuArgLeuProHisSerThrLeuArgCysAlaAsnIleThrIle 200
 DB 550 AGCAGCTCCAGCCCGCCAGTGTAGCGCTGCTTCACACCTTCGATGGGCCAATCCATC 609
 QY 201 IleGlnHisGlnLysCysGlnAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220
 DB 610 ATTGAGCACAGAAAGTGTAGAAACGCGTACCCCGGGAACATCACAGACCATGTGGTGT 669
 QY 221 AlaSerValGlnGlnGlyGlyLysAspSerCysGlnGlyAspSerGlyGlyProLeuVal 240
 DB 670 GCCACCGTGCAGAAAGGGGGAAGAGACTCTCCACGGGGGACTCCGGGGGCCCTTGTGTC 729
 QY 241 CysAsnGlnSerLeuGlnGlyIleIleSerTrrpGlyGlnAspProCysAlaIleThrArg 260
 DB 730 TGTATCCACTCTCTTCAAGCGATTATCTCTGGGGCCAGATCCGTGTGCCATCCCGA 789
 QY 261 LysProGlyValTrrpThrLysValCysLysTrrpLysAspTrrpIleGlnGlnThrMetLys 280
 DB 790 AAGCTGTGGTGTACACGAAAGTGTGAAATATGTGACTGGATCCAGAGACGATGAAG 849
 QY 281 AsnAsn 282
 DB 850 AACCAAT 855
 DB 16-MAY-2002 (first entry)
 DE Human PRO1279 cDNA sequence SEQ ID NO:207.
 XX ABL88175 standard; cDNA, 1204 BP.
 XX ABL88175;
 XX Human PRO1279 cDNA sequence SEQ ID NO:207.
 XX Human; angiogenesis; cardiac; cytosolic; antiangiogenic; hypotensive;
 KW human; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
 KW age-related macular degeneration; arterial restenosis; angina;
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 KW wound healing; chromosome mapping; gene mapping; gene; ss.
 OS Homo sapiens.
 XX

PN W0200200650-A2.
 XX 03-JAN-2002.
 PD 20-JUN-2001; 2001WO-US19692.
 XX 23-JUN-2000; 2000US-213637P.
 PR 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 02-AUG-2000; 2000US-222695P.
 PR 17-AUG-2000; 2000US-0643657.
 PR 23-AUG-2000; 2000WO-US33522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 07-SEP-2000; 2000US-230978P.
 PR 18-SEP-2000; 2000US-0664610.
 PR 18-SEP-2000; 2000US-0665350.
 PR 24-OCT-2000; 2000US-242922P.
 PR 08-NOV-2000; 2000US-0709238.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 22-JAN-2001; 2001US-0767609.
 PR 28-FEB-2001; 2001US-0796498.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0808689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 30-MAY-2001; 2001US-0870574.
 PR 30-MAY-2001; 2001WO-US17443.
 PR 01-JUN-2001; 2001WO-US17800.
 XX
 PA (GENENTECH INC.
 XX Baker KP, Ferrara N, Gerber H, Gertlisen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 XX WPI; 2002-090516/12.
 DR P-PsDB; ABB84920.
 XX
 PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal -
 XX
 XX Claim 2; Fig 207; 565pp; English.
 XX
 XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
 CC ABB85003. The PRO proteins and polynucleotides have cardiac, cytosolic,
 CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
 CC activities, and can be used in gene therapy. The PRO polynucleotides,
 CC proteins, agonists and antagonists are useful for treating or diagnosing
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal,
 CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular
 CC degeneration, atherosclerosis, hypertension, arterial restenosis,
 CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
 CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
 CC carcinoma) and wound healing. The PRO polynucleotides have applications
 CC in molecular biology, including use as hybridisation probes, and in
 CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
 CC probes used in the exemplification of the present invention.
 XX
 XX Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;

Alignment Scores:

Pred. No.: 2,5e-122 Length: 1204
 Score: 1523.00 Matches: 282
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0

US-09-856-320A-2 (1-282) x ABK3628 (1-1204)

```

QY 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyValArgGlyLeuThrAlaAla 20
DB 10 ATGCAAGAGGTGGAGGTGGCTGCGGAGCTGGAAGTCATCGGGCAGAGGTCTCAGCAGAGCC 69
QY 21 LysGluProGlyValAlaArgSerProLeuGlnAlaMetArgIleLeuGlnLeuIleLeu 40
DB 70 AAGGAACCTGGGGCGGCTCTCCCTCCAGGCGCATGAGATTCTGCAAGTTAATCCCTG 129
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyValThrArgIleIleLysGlyPheGluCys 60
DB 130 CTTCCTCTGGCAACAGGCTTGTAGGGGAGAGACCAAGATCATCAAGGGGTTCCAGTCC 189
QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlyIleThrArgLeuLeuCysGly 80
DB 190 AAGCTCAGCTCCAGGCTGGCAGGAGCCCTGTCGAGAGAAGCGCGCTACTCTGTGG 249
QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
DB 250 GGCAGCCTATGCGCCCGAGATGGCTCCGACAGCAGCCAGCTCCCAAGCCCGCTAC 309
QY 101 IleValHisLeuGlyValHisLeuGlnGlyGlyValCysGlyGlnThrArgTrp 120
DB 310 ATAGTTACACTGGGGAGAGACAACCTCCAGGAAGAGAGAGGCTGTAGCAGACCCGAGACA 369
QY 121 AlaThrGluSerPheProHisSerProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
DB 370 GGCAGTGAATCTCTCCCGCAGCCGCTTCAACAACAGGCTCCCAACAAGCCAGCCG 429
QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
DB 430 AATGACATCATCTGTGTGAAGATGGCATGCGACATCCATCATCAAGGCTGTGGAGACC 489
QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
DB 490 CTCACCTCTCTCTCAGCTGTGTCTACTGCTGGACACAGCTGCTCTATTCGCGCTGGGC 549
QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
DB 550 AGCAGCTCCAGCCCGCAGTTACGCTGCGCTCAGACACTTGCATGGCCCAACATCAACATC 609
QY 201 IleGluHisGlnLysGlyLysAsnAlaIleTrpGlyValAsnIleThrAspThrMetValCys 220
DB 610 ATTGAGACACAGAAAGTGAAGAACGCTTACCCCGGACATCAACAGACCCATGTGGTGT 669
QY 221 AlaSerValGlnGlyValLysAspSerCysGlnGlyAspSerGlyValProLeuVal 240
DB 670 GCCACGCTGCAAGAGGGGCAAGACCTCTGCGAGGAGTCTCGGGGGCCCTCTGGTC 729
QY 241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyValAspProCysAlaIleThrArg 260
DB 730 TGTAAACAGTCTCTCAAGGATTAATCTCTGGGGCAGAGATCCGTTGCGATCAACCGCA 789
QY 261 LysProGlyValIleThrLysValCysLysTyrValAspTrpIleGlnGlnThrMetLys 280
DB 790 AAGCCGTGGTGTACACGAAGCTTGCATAATGTGACTGATCAGAGAGCGATGAAG 849
QY 281 AsnAsn 282
DB 850 AACCAAT 855

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ID ABK3628 standard; cDNA; 1204 BP.
AC ABK3628;
XX
XX 08-MAY-2002 (first entry)
DT
XX cDNA encoding human PRO protein, Seq ID No 185.
XX
DE
XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
XX breast cancer; prostate tumour; rectal tumour; liver tumour;
XX pericyte cell proliferation; chondrocyte cell proliferation;
XX tumour necrosis factor-alpha; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200208288-A2.
XX
PD 31-JAN-2002.
XX
PF 29-JUN-2001; 2001WO-US21066.
XX
PR 20-JUL-2000; 2000US-219556P.
XX
PR 25-JUL-2000; 2000US-220585P.
XX
PR 25-JUL-2000; 2000US-220605P.
XX
PR 25-JUL-2000; 2000US-220607P.
XX
PR 25-JUL-2000; 2000US-220624P.
XX
PR 25-JUL-2000; 2000US-220638P.
XX
PR 25-JUL-2000; 2000US-220664P.
XX
PR 25-JUL-2000; 2000US-220666P.
XX
PR 26-JUL-2000; 2000US-220893P.
XX
PR 28-JUL-2000; 2000WO-US20710.
XX
PR 23-AUG-2000; 2000WO-US23522.
XX
PR 24-AUG-2000; 2000WO-US23328.
XX
PR 15-SEP-2000; 2000US-000000P.
XX
PR 10-NOV-2000; 2000WO-US30873.
XX
PR 28-NOV-2000; 2000US-253646P.
XX
PR 01-DEC-2000; 2000WO-US33678.
XX
PR 20-DEC-2000; 2000US-0747259.
XX
PR 20-DEC-2000; 2000WO-US34956.
XX
PR 28-FEB-2001; 2001WO-US06520.
XX
PR 10-MAY-2001; 2001US-0854280.
XX
PR 25-MAY-2001; 2001WO-US17092.
XX
PA (GERTH ) GENENTECH INC.
XX
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2002-172001/22.
XX
XX P-PSDB; AMU83684.
XX
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
XX useful for treating a PRO related disorder and for diagnosing tumours
XX such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
XX tumour or liver tumour -
XX
XX Claim 2; Figure 185; 359pp; English.
XX
XX The invention relates to one hundred and twenty two nucleic acids
XX encoding PRO polypeptides. The sequences of the 122 PRO polypeptides
XX encode human secreted proteins. The PRO nucleic acids, polypeptides,
XX agonists and antagonists are useful for treating a PRO related disorder.
XX The PRO polypeptides are useful for diagnosing tumours, especially lung
XX cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
XX liver tumour. The PRO polypeptides are useful for stimulating the
XX proliferation of, or gene expression, in pericyte cells, for stimulating
XX the proliferation or differentiation of chondrocyte cells, for
XX stimulating the release of tumour necrosis factor-alpha from human blood,
XX for stimulating or inhibiting the proliferation of normal human dermal
XX fibroblast cells. The PRO polypeptide may also be used as molecular
XX weight markers and for tissue typing. The PRO nucleic acids have
XX applications in molecular biology, including use as hybridisation probes,
XX and in chromosome and gene mapping. ABK3536-ABK3657 represent human
XX

```

CC PRO protein coding sequences of the invention.

XX Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;

SQ

Alignment Scores:

Pred. No.:	2	5e-122	Length:	1204
Score:	1523.00		Matches:	282
Percent Similarity:	100.00%		Conservative:	0
Best Local Similarity:	100.00%		Mismatches:	0
Query Match:	100.00%		Indels:	0
DB:	24		Gaps:	0

US-09-856-320A-2 (1-282) x ABK33628 (1-1204)

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QY 1 MetGlnArgLeuArgTyrPleuArgAspTyrPlySserSerGlyArgGlyLeuThrAlaAla 20
DB 10 ATGCAGAGGTTGAGGTGCTCGCGGAGTGAAGTCATCGGCAGAGGTCTCACAGAGCC 69
QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuLeu 40
DB 70 AAGGAACCTGGGCGCTCTCTCCCTCCAGGCCATGAGATTCTGCGATTAAATCTTG 129
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyIleThrArgIleIleLeuGlyPheGlyCys 60
DB 130 CTTCCTCTGGCAACAGGCTTTCAGGGGAGAGACCAGATCATCAGGGCTTCAGATCC 189
QY 61 LysProHisSerGlnProTyrGlnAlaAlaLeuPheGlyIleThrArgLeuLeuCysGly 80
DB 190 AAGCTCACTCCAGCCCTGCGAGGAGCCCTGTTGAGAGACGGGGCTACTGTGGG 249
QY 81 AlaThrLeuIleAlaProArgTyrPleuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
DB 250 GCGAGCTCATGCCCCCAGATGGCTCTCGACAGACGCCCTCAAGCCCGCTAC 309
QY 101 IleValHisLeuGlyGlnHisLeuGlnGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 120
DB 310 AATGTTCACTGGGCGAGCAACACTCCGAAAGAGAGGGCTGTGAGAGACCCGGACA 369
QY 121 AlaThrGlnSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
DB 370 GCACAGATCTCTCCCCCAGCCCGCTTCACAAACAGCCCTCCCAACAAAGACACCGC 429
QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTyrAlaValArgPro 160
DB 430 AATGACATCATCTGCTGAAGATGCGATCGCAGTCTCATCACTGGCTGTGGACCC 489
QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTyrGly 180
DB 490 CTCACCTCTCTCTACGCTGTCTCACTGCTGSCACACAGCTGCTCATTTCCGGCTGGGG 549
QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
DB 550 AGCAGCTCCAGCCCGCAGTTACGCTGCTCCTCACACCTTCGATGCGCAACATCACATC 609
QY 201 IleGlnHisGlnLysCysGlnAsnAlaTyrProGlyAsnIleThrAspThrMetAlaCys 220
DB 610 ATTGGACACAGAGATGTGAGAACGCTACCCCGGACATACAGACACCATGGTGTGT 669
QY 221 AlaSerValGlnGlyGlyLysAspSerCysGlnGlyLysAspSerGlyGlyProLeuVal 240
DB 670 GCCACGCTGCAGGAAGGGGCGAAGACTCTCTCCAGGGTGAATCCGGGGGCCCTCTGCTC 729
QY 241 CysAsnGlnSerLeuGlnGlyIleIleSerTyrGlyGlnAspProCysAlaIleThrArg 260
DB 730 TGTAAACAGCTCTCTCAAGGCAATATCTCTGGGGCCAGAGATCCGTGTGCGATCACCGGA 789
QY 261 LysProGlyValTyrThrLysValCysLysTyrValAspTyrIleGlnIleThrMetLys 280
DB 790 AAGCTGTGTCTACACGAAGTCTGCAAAATATGTGAGCTGTGATCCAGAGACGATGAG 849
QY 281 AsnAsn 282
DB 850 AACCAAT 855
```

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RESULT 11
ID ACA03855
ID ACA03855 standard; cDNA; 1204 BP.
AC ACA03855;
XX 23-MAY-2003 (first entry)
XX 23-MAY-2003 (first entry)
DE cDNA encoding human PRO polypeptide #253.
XX cDNA encoding human PRO polypeptide #253.
XX Human; PRO polypeptide; secreted and transmembrane protein;
XX tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
XX differentiation; chondrocyte; tumour; genetic disorder;
XX cytosolic; gene; ss.
XX Homo sapiens.
XX
XX US2003036180-A1.
XX
XX 20-FEB-2003.
XX
XX 09-MAY-2002; 2002US-0143114.
XX
XX 31-MAR-1997; 97WO-US05230.
XX
XX 12-JUN-1998; 98WO-US12456.
XX
XX 14-JUL-1998; 98WO-US14552.
XX
XX 28-AUG-1998; 98WO-US17888.
XX
XX 10-SEP-1998; 98WO-US18824.
XX
XX 14-SEP-1998; 98WO-US19099.
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XX 14-SEP-1998; 98WO-US19099.
XX
XX 14-SEP-1998; 98WO-US19177.
XX
XX 16-SEP-1998; 98WO-US19330.
XX
XX 17-SEP-1998; 98WO-US19437.
XX
XX 07-OCT-1998; 98WO-US21141.
XX
XX 29-OCT-1998; 98WO-US22991.
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XX 29-OCT-1998; 98WO-US22992.
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XX 20-NOV-1998; 98WO-US24855.
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XX 01-DEC-1998; 98WO-US25108.
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XX 05-JAN-1999; 99WO-US00106.
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XX 08-MAR-1999; 99WO-US05028.
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XX 10-MAR-1999; 99WO-US05190.
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XX 20-APR-1999; 99WO-US08615.
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XX 14-MAY-1999; 99WO-US10733.
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XX 02-JUN-1999; 99WO-US12252.
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XX 01-SEP-1999; 99WO-US20111.
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XX 08-SEP-1999; 99WO-US20594.
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XX 13-SEP-1999; 99WO-US20944.
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XX 15-SEP-1999; 99WO-US21090.
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XX 15-SEP-1999; 99WO-US21547.
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XX 05-OCT-1999; 99WO-US23089.
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XX 29-NOV-1999; 99WO-US28214.
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XX 30-NOV-1999; 99WO-US28313.
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XX 30-NOV-1999; 99WO-US28409.
XX
XX 01-DEC-1999; 99WO-US28301.
XX
XX 01-DEC-1999; 99WO-US28634.
XX
XX 02-DEC-1999; 99WO-US28551.
XX
XX 02-DEC-1999; 99WO-US28564.
XX
XX 02-DEC-1999; 99WO-US28565.
XX
XX 16-DEC-1999; 99WO-US30095.
XX
XX 20-DEC-1999; 99WO-US30911.
XX
XX 20-DEC-1999; 99WO-US30999.
XX
XX 22-DEC-1999; 99WO-US30720.
XX
XX 30-DEC-1999; 99WO-US31243.
XX
XX 05-JAN-2000; 99WO-US31274.
XX
XX 05-JAN-2000; 2000WO-US00219.
XX
XX 06-JAN-2000; 2000WO-US00277.
XX
XX 06-JAN-2000; 2000WO-US00376.
XX
XX 11-FEB-2000; 2000WO-US03565.
XX
XX 18-FEB-2000; 2000WO-US04341.
XX
XX 18-FEB-2000; 2000WO-US04342.
XX
XX 22-FEB-2000; 2000WO-US04414.
XX
XX 24-FEB-2000; 2000WO-US04914.
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24-FEB-2000; 2000MO-US05004.
 PR 01-MAR-2000; 2000MO-US05601.
 PR 02-MAR-2000; 2000MO-US05746.
 PR 02-MAR-2000; 2000MO-US05841.
 PR 10-MAR-2000; 2000MO-US06319.
 PR 15-MAR-2000; 2000MO-US06884.
 PR 20-MAR-2000; 2000MO-US07377.
 PR 21-MAR-2000; 2000MO-US07532.
 PR 30-MAR-2000; 2000MO-US08439.
 PR 17-MAY-2000; 2000MO-US13705.
 PR 22-MAY-2000; 2000MO-US14042.
 PR 30-MAY-2000; 2000MO-US14941.
 PR 02-JUN-2000; 2000MO-US15264.
 PR 28-JUL-2000; 2000MO-US20710.
 PR 11-AUG-2000; 2000MO-US22031.
 PR 23-AUG-2000; 2000MO-US23322.
 PR 24-AUG-2000; 2000MO-US23328.
 PR 08-NOV-2000; 2000MO-US30952.
 PR 10-NOV-2000; 2000MO-US30873.
 PR 01-DEC-2000; 2000MO-US32678.
 PR 20-DEC-2000; 2000MO-US34956.
 PR 28-FEB-2001; 2001MO-US06520.
 PR 01-MAR-2001; 2001MO-US06666.
 PR 25-MAY-2001; 2001MO-US17092.
 PR 01-JUN-2001; 2001MO-US17800.
 PR 20-JUN-2001; 2001MO-US19692.
 PR 22-JUN-2001; 2001MO-US20116.
 PR 29-JUN-2001; 2001MO-US21066.
 PR 09-JUL-2001; 2001MO-US21735.
 PR 20-DEC-2000; 2000MO-US21735.
 PR 28-FEB-2001; 2001US-0796498.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0806869.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854280.
 PR 10-MAY-2001; 2001US-0854280.
 PR 18-MAY-2001; 2001US-0860216.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 01-JUN-2001; 2001US-0872035.
 PR 05-JUN-2001; 2001US-0874503.
 PR 14-JUN-2001; 2001US-0882636.
 PR 19-JUN-2001; 2001US-0886342.
 PR 21-JUN-2001; 2001US-0887879.
 PR 18-JUL-2001; 2001US-0908827.
 PR 06-AUG-2001; 2001US-0924419.
 PR 09-AUG-2001; 2001US-0927796.
 PR 16-AUG-2001; 2001US-0931836.
 PR 19-DEC-2001; 2001US-0028072.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 DR WPI, 2003-332040/31.
 DR P-PSDB; ABU6822.
 PT New secreted and transmembrane PRO nucleic acids, useful for gene
 PT therapy, in chromosome and gene mapping, as chromosome markers, in
 PT tissue typing, and in chromosome identification.
 XX
 PS Claim 2: Fig 505; 660pp; English.
 XX
 CC The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The
 CC PRO polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides are useful for detecting other PRO polypeptides, for
 CC linking bioactive molecules to cells expressing PRO polypeptides,
 CC for modulating biological activities of cells expressing PRO
 CC polypeptides, and for identifying agonists or antagonists.

CC The PRO polypeptides are useful for stimulating the release of
 CC tumour necrosis factor (TNF)-alpha from human blood, for stimulating
 CC the proliferation or differentiation of chondrocytes, and detecting the
 CC presence of tumours. The polynucleotide sequences encoding PRO
 CC polypeptides are useful as hybridisation probes, in chromosome and
 CC gene mapping, in the generation of antisense RNA and DNA, in the
 CC preparation of PRO polypeptides, for generating transgenic animals or
 CC knockout animals, for the genetic analysis of individuals with genetic
 CC disorders, and in gene therapy. ACN03603;ACN03877 represent cDNAs
 CC encoding the human PRO polypeptides of the invention.
 CC Note: The sequence data for this patent was obtained in electronic
 CC format directly from the USPTO web site at
 CC segdata.uspto.gov/psipspidEntry.html.
 XX
 SQ Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;
 Alignment Scores:
 Pred. No.: 2,5e-122 Length: 1204
 Score: 1523.00 Matches: 282
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 25 Gaps: 0
 US-09-856-320A-2 (1-282) x ACA03855 (1-1204)
 QY 1 MetGlnArgLeuArgTyrPheuArgAspTyrLysSerSerGlyArgGlyLeuThrAlaAla 20
 DB 10 ATGCAGAGAGTTGAGGTGCTGCGGAGATGGAAGTATCATGGGAGAGTCTCACACAGCC 69
 QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleu 40
 DB 70 AAGGAACCTGGGGCCCGCTCTCCCTCCAGGCGCATGAGGATTTGAGTTAAATCTG 129
 QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyGluThrArgIleIleLeuGlyPheGlyCys 60
 DB 130 CTTCCTCTGGCAACAGGGGCTGTAGGGAGAGACAGAGATCATCAAGGGTTCCAGTCC 189
 QY 61 LysProHisSerGlnProTyrGlnAlaAlaLeuPheGlyLysThrArgLeuLeuCysGly 80
 DB 190 AAGCTCTACCTCCAGCCCTGCGAGGACAGCCCTGTTCGAGAGACCCGCTACTCTGTGG 249
 QY 81 AlaThrLeuIleAlaProArgTyrPheLeuThrAlaAlaHisCysLeuLysProArgTyr 100
 DB 250 GCGACGCTCATCGCCCGCAGATGGCTCTGACAGAGCCACTGCTCAAGCCCGCTAC 309
 QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGluGluGlyCysGluGlnThrArgThr 120
 DB 310 ATAGTTCACTGGGGCAGACACACTCCAGAAAGGAGGGGCTGTGACAGACCCGGACA 369
 QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
 DB 370 GCCACTGAGTCTTCCCTCCACCCCGGCTTCAACAAACACCTCCCAACAAAGACACCGC 429
 QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
 DB 430 AATGACATCATGTGGTGAAGATGGATCGACAGCTTCATCATCTGAGCTGTGGACCC 489
 QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTyrGly 180
 DB 490 CTCACCTCTCTCTCAGCTGTGTCTACCTGTCAGCAGCTGCTCATTTCCGGCTGGGGC 549
 QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
 DB 550 AGCAGCTCCACCCCGCTTACGCTGCTGCACACCTTCATGCGCAATCATCCACATC 609
 QY 201 IleGluHisGlnLysCysGluAsnAlaThrProGlyAsnIleThrAspThrMetValLys 220
 DB 610 ATTGAGCACCAAGATGTGAAGACGCTTACCCGGCAACATCATCAGACACATGAGTGT 669
 QY 221 AlaSerValGlnGluGlyLysAspSerCysGlnGlyAspSerGlyLysProLeuVal 240
 DB 670 GCCAGCGTGCAGAGGGGGCAGAGGATCTCTGCCAGGGTGACTCCGGGGCTCTGTGTC 729

QY 241 CysAengInserLeuGInGlyIleIleSerTpgIyGInAspProCyAlaIleThrArg 260
Db 730 TGTAAcCGATCTCTTCAAGGCAATTATCTCTGGGCGCAGATCCGTGTGCATCACCCGA 789
QY 261 LysProGlyValIlyThrIysValCysLysTyrValAspTrpIleGInGInThrMetLys 280
Db 790 AAGCTGTGTCTACACGAAAGTCTGCATATATGTGACTGATCCAGAGACGATGAAG 849
QY 281 AsnAsn 282
Db 850 AACCAAT 855
RESUT 12
ACA04276
ID ACA04276 standard; cDNA; 1204 BP.
XX ACA04276;
AC 27-MAY-2003 (first entry)
XX
DT Human cDNA encoding a secreted/transmembrane protein, SEQ ID 505.
XX
DE
XX Human; ss; gene; secreted protein; transmembrane protein; PRO;
KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;
KW infertility; birth defects; premature aging; AIDS; biosensor;
KW acquired immunodeficiency syndrome; cancer; diabetic complication;
KW bioreactor; tumour.
XX
OS Homo sapiens.
XX US2003032155-A1.
XX
XX 13-FEB-2003.
XX
XX 03-MAY-2002; 2002US-0137865.
XX
XX 31-MAR-1997; 97WO-US05230.
PR 12-JUN-1996; 98WO-US12456.
PR 14-JUL-1996; 98WO-US14552.
PR 28-AUG-1996; 98WO-US17888.
PR 10-SEP-1996; 98WO-US18824.
PR 14-SEP-1996; 98WO-US19093.
PR 14-SEP-1996; 98WO-US19094.
PR 14-SEP-1996; 98WO-US19177.
PR 16-SEP-1996; 98WO-US19330.
PR 17-SEP-1996; 98WO-US19437.
PR 07-OCT-1996; 98WO-US21141.
PR 29-OCT-1996; 98WO-US22991.
PR 29-OCT-1996; 98WO-US22992.
PR 20-NOV-1996; 98WO-US24855.
PR 01-DEC-1996; 98WO-US25108.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99WO-US05190.
PR 20-APR-1999; 99WO-US08615.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28409.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.

PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 22-DEC-1999; 99WO-US30720.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05746.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 22-JUN-2001; 2001WO-US20116.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 20-DEC-2000; 2000US-0747259.
PR 28-FEB-2001; 2001US-0796498.
PR 09-MAR-2001; 2001US-0802708.
PR 12-MAR-2001; 2001US-0808689.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 18-MAY-2001; 2001US-0860216.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0883642.
PR 21-JUN-2001; 2001US-0887879.
PR 18-JUL-2001; 2001US-0908827.
PR 06-AUG-2001; 2001US-0924419.
PR 09-AUG-2001; 2001US-0927796.
PR 16-AUG-2001; 2001US-0931836.
PR 19-DEC-2001; 2001US-0028072.
XX
XX (GENTH) GENENTECH INC.
XX
XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
PI Gertlisen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-331925/31.
XX P-PSDB; ABU67098.

PT New secreted and transmembrane nucleic acids and polypeptides,
 PT designated as PRO, useful for treating inflammation, organ failure,
 PT atherosclerosis, cardiac injury, infertility, birth defects, premature
 PT aging, AIDS, or cancer

PS Claim 2; Fig 505; 659pp; English.

XX
 CC The invention relates to an isolated nucleic acid comprising, or which is
 CC at least 80% identical to, or the full-length coding sequence of, any of
 CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
 CC (one of 275 secreted or transmembrane proteins). The nucleic acid
 CC further comprises the full-length coding sequence of the DNA deposited
 CC under American Type Culture Collection (ATCC) accession number in a list
 CC given in the specification. Also included are vectors and host
 CC cells for producing PRO proteins, PRO fusion proteins, anti-PRO
 CC antibodies, PRO extracellular domains and mature sequences, methods
 CC of detecting PRO proteins, methods for stimulating the release of
 CC TNF-alpha (tumor necrosis factor alpha) from human blood,
 CC (and the proliferation of differentiation of chondrocyte cells, the release or
 CC proliferation of, or gene expression in pericyte cells, the release or
 CC proteoglycans from cartilage, proliferation of inner ear utricular
 CC supporting cells, the proliferation of T-lymphocyte cells, the release
 CC of a cytokine from peripheral blood mononuclear cells (PBMC), or the
 CC proliferation of endothelial cells), a method for modulating the uptake
 CC of glucose or free fatty acid (FFA) by skeletal muscle cells,
 CC a method for inhibiting the binding of A-peptide to factor VIIA,
 CC or the differentiation of adipocyte cells, a method for detecting the
 CC presence of a tumor in a mammal and an oligonucleotide probe derived
 CC from any of the nucleotide sequences cited above. The nucleic acids and
 CC polypeptides are useful for treating inflammatory diseases, organ
 CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
 CC premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or
 CC diabetic complications. The nucleic acids are useful as hybridization
 CC probes, in chromosome and gene mapping, and in generating antisense RNA
 CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,
 CC biosensors or bioreactors. Both are useful in tissue typing.
 CC The present sequence encodes a PRO protein of the invention.

XX
 XX Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;

Alignment Scores:

Pred. No.: 2,5e-122 Length: 1204
 Score: 1523.00 Matches: 282
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 25 Gaps: 0

US-09-856-320A-2 (1-282) x ACA04276 (1-1204)

QY 1 MetGlnArgLeuAArgTrrpleuAArgaPTrrpLysSerSerGlyAArgGlyLeuThraAla 20
 DB 10 ATGCAAGAGTTAGAGGGCTGGCGGCTGGAAGTCACTCGGAGAGAGTCTCAGAGGCC 69
 QY 21 LysGluProGlyAlaAArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeu 40
 DB 70 AAGGAACCTGGGGCCGCTCTCCCTCCAGGCCATAGAGTTCTGAGTTAATCTG 129
 QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyIuThraArgIleIleLysGlyPheGlyCys 60
 DB 130 CTTCCTCTGGCAACAGGCTTGTAGGGGAGAGACCAGATCATCAAGGGTTCCAGTGC 189
 QY 61 LysProHisSerGlnProTrrpGlnAlaAlaLeuPheGlnIuThraArgLeuLeuCysGly 80
 DB 190 AAGCTCACTCCAGCCCTGGCAGGAGCCCTGTTGCAAAACGCGGCTACTCTGTGGG 249
 QY 81 AlaThrLeuIleAlaProArgTrrpleuLeuThraAlaHisCysLeuLysProArgTyr 100
 DB 250 GGCAGCCTCATGCCGCCGAGATGGCTCTCGACAGCAGCCCATCTGCTCAAGCCCGCTAC 309
 QY 101 IleValHisLeuGlyGlnHisLeuGlnIuThraArgGlyCysGlnIuThraArgThr 120
 DB 310 ATAGTTCACTGGGGGAGCACAACCTCCAGAGAGAGAGGGCTGTGTAGCAGACCCGGACA 369

QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
 DB 370 GCCACTGAGTCTTCCCCCAACCCGGCTTCAACACAGCTCTCCCAACAAGCCACCCG 429
 QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
 DB 430 AATGACATATCTGTTGAAGATGGCATGCCAGTCTCATCATCGGGCTGTGGACCC 489
 QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrrpGly 180
 DB 490 CTCACCTCTCTCCACGCTGTCTCACTGCTGGCAGCAGCTGCTCATTTCCGCTGGGGC 549
 QY 181 SerThrSerSerProGlnLeuArgLeuProHisIleThrLeuArgCysAlaAsnIleThrIle 200
 DB 550 ACGAGCTCCAGCCCGCCAGTTACGCTGCTTCAACACTTGCATGGCCCAACATCACCATT 609
 QY 201 IleGluHisLeuGlyCysGlnAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220
 DB 610 ATTGAGCACCAGAAAGTGTAGAACCGCTTACCCCGGCAACATCAGACACCATGCTGTGT 669
 QY 221 AlaSerValGlnGlyGlyIuThraAspSerCysGlnIuThraAspSerGlyIuProLeuVal 240
 DB 670 GCAGGCTGCAGAAAGGGGCAAGGACTCTCCAGGGTGACTCCGGGGGCTCTGTGTC 729
 QY 241 CysAsnGlnSerLeuGlnGlyIleIleSerTrrpGlnAspProCysAlaIleThrArg 260
 DB 730 TTTAACCACTCTCTTCAAGCATTTATCTCTGGGCGCAGATTCGTTGCGATCACCCTGA 789
 QY 261 LysProGlyValTyrThrLysValCysLysTyrValAspTrrpIleGlnIuThraMetLys 280
 DB 790 AAGCTGGGTGTACACGAAACTTGCAAATATGTGGATGTGATCAGAGAGCATGAAG 849
 QY 281 AsnAsn 282
 DB 850 AACCAAT 855

RESULT 13
 ABX89393
 ID ABX89393 standard; cDNA; 1204 BP.
 AC ABX89393;
 XX
 DT 13-MAY-2003 (first entry)
 XX
 DE DNA encoding novel secreted and transmembrane protein PRO1279.
 XX
 KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
 KW cardiac insufficiency disorder; cancer; tumor; immune response;
 KW adrenal cortical capillary endothelial growth; c-fos induction;
 KW vascular endothelial growth factor inhibitor; T-lymphocytes stimulation;
 KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
 KW retinal neurons cell survival; rod photoreceptor cell survival;
 KW retinal disorder; retinitis pigmentosa; kidney disorder;
 KW mammalian kidney mesangial cell proliferation; Berger disease;
 KW dermatitis; herpeticiforms; Crohn's disease; chondrocyte proliferation;
 KW chondrocyte redifferentiation; sports injury; arthritis; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2003017563-A1.
 XX
 PD 23-JAN-2003.
 XX
 PF 07-MAY-2002; 2002US-0140808.
 XX
 PR 31-MAR-1997; 97WO-US05230.
 PR 12-JUN-1998; 98WO-US12456.
 PR 14-JUL-1998; 98WO-US14552.
 PR 28-AUG-1998; 98WO-US17888.
 PR 10-SEP-1998; 98WO-US18824.
 PR 14-SEP-1998; 98WO-US19093.
 PR 14-SEP-1998; 98WO-US19094.

PR 14-SEP-1998; 98WO-US19177.
 PR 16-SEP-1998; 98WO-US19330.
 PR 17-SEP-1998; 98WO-US19437.
 PR 07-OCT-1998; 98WO-US21141.
 PR 29-OCT-1998; 98WO-US22991.
 PR 29-OCT-1998; 98WO-US22992.
 PR 20-NOV-1998; 98WO-US24855.
 PR 01-DEC-1998; 98WO-US25108.
 PR 05-JAN-1999; 99WO-US00106.
 PR 08-MAR-1999; 99WO-US05028.
 PR 10-MAR-1999; 99WO-US05190.
 PR 20-APR-1999; 99WO-US08615.
 PR 14-MAY-1999; 99WO-US10733.
 PR 02-JUN-1999; 99WO-US12252.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 13-SEP-1999; 99WO-US20944.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 05-OCT-1999; 99WO-US23089.
 PR 29-NOV-1999; 99WO-US28214.
 PR 30-NOV-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28409.
 PR 01-DEC-1999; 99WO-US28301.
 PR 02-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28564.
 PR 02-DEC-1999; 99WO-US28565.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 20-DEC-1999; 99WO-US30999.
 PR 22-DEC-1999; 99WO-US30720.
 PR 30-DEC-1999; 99WO-US31243.
 PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 02-MAR-2000; 2000WO-US05746.
 PR 10-MAR-2000; 2000WO-US05841.
 PR 15-MAR-2000; 2000WO-US06319.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 11-AUG-2000; 2000WO-US22031.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 22-JUN-2001; 2001WO-US20116.
 PR 29-JUN-2001; 2001WO-US21066.
 PR 09-JUL-2001; 2001WO-US21735.
 PR 20-DEC-2000; 2000US-0747259.
 PR 28-FEB-2001; 2001US-0796498.

PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0808689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 18-MAY-2001; 2001US-0860216.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 01-JUN-2001; 2001US-0872035.
 PR 05-JUN-2001; 2001US-0874503.
 PR 14-JUN-2001; 2001US-0882636.
 PR 19-JUN-2001; 2001US-0886342.
 PR 21-JUN-2001; 2001US-0887879.
 PR 18-JUL-2001; 2001US-0908827.
 PR 06-AUG-2001; 2001US-0924419.
 PR 09-AUG-2001; 2001US-0927796.
 PR 16-AUG-2001; 2001US-0931836.
 PR 19-DEC-2001; 2001US-0028072.
 XX
 XX (GETH) GENENTECH INC.
 PA Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerlitsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX WPI; 2003-148238/14.
 DR P-Psdb; ABUS9903.
 XX
 XX
 PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
 PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
 PT are therapeutically useful for enhancing immune response and in cancer
 PT treatments
 XX
 PS Claim 2; Fig 505; 659pp; English.
 XX
 CC The invention describes an isolated human PRO polypeptide. The PRO
 CC polypeptides are useful in detecting PRO polypeptides in a sample, in
 CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
 CC in modulating at least one biological activity of a cell expressing a PRO
 CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
 CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
 CC stimulate adrenal cortical capillary endothelial growth and PRO536,
 CC PRO943, PRO828, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
 CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
 CC useful for treating conditions or disorders where angiogenesis would be
 CC beneficial, e.g. wound healing and antagonist of this polypeptide are
 CC useful for treating cancerous tumours. PRO812 inhibits vascular
 CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
 CC cells and is thus useful for inhibiting endothelial cell growth in
 CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
 CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
 CC stimulated T-lymphocytes and are therapeutically useful for enhancing
 CC immune response. PRO828, PRO826, PRO1068 or PRO132 enhance survival of
 CC retinal neurons cells (PRO132 is also enhances survival/proliferation of
 CC rod photoreceptor cells) and therefore are useful for treating retinal
 CC disorders of injuries, e.g. retinitis pigmentosa. AND. PRO819, PRO813
 CC and PRO1106 induce proliferation of mammalian kidney mesangial cells,
 CC and therefore are useful for treating kidney disorders associated with
 CC decreased mesangial cell function such as Berger disease or other
 CC nephropathies associated with dermatitis, herpeticiforms or Crohn's
 CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
 CC proliferation and/or redifferentiation of chondrocytes in culture and
 CC are thus useful for treating sports injuries, and arthritis. This
 CC sequence encodes a novel human PRO protein.
 XX
 SQ Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;
 Alignment Scores:
 Pred. No.: 2.5e-122 Length: 1204
 Score: 1523.00 Matches: 282
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
 DB: 25 Gaps: 0
 US-09-856-320A-2 (1-282) x ABX89393 (1-1204)

```

QY 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAla 20
DB 10 ATGCAAGAGTTGAGTGGCTGGCGGACTGGAAGTCACTCCGGCAGAGTCTCACAGCAGCC 69
QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgLLeuGlnLeu 40
DB 70 AAGGAACCTGGGGCCGCTCTCCCTCCAGGCAATGAGATTGCAAGTTAATCTG 129
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyLeuThrArgLLeuGlyPheGlyCys 60
DB 130 CTTCCTCTGGCAACAGGCTTTGAGGGAGAGACCAAGATCAAGAGGATTCGAGTCC 189
QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlyLysThrArgLeuLeuCysGly 80
DB 190 AAGCTCACTCCAGCCCTGGCAGGCACTGTTGAGAGACCGGCTACTCTGTGG 249
QY 81 AlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
DB 250 GCGAGCTCATGCGCCCGCAGATGGCTCTGACAGCAGCCACCTGCTCAAGCCCGCTAC 309
QY 101 LLeuAlaHisLeuGlyGlnHisAsnLeuGlnLysGlyGlyGlyGlnGlnThrArgThr 120
DB 310 ATAGTTCACTGGGAGACACACCTCCAGAGAGAGAGGAGGCTGTGAGACAGACCGGACA 369
QY 121 AlaThrGlySerPheProHisSerProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
DB 370 GGCAGTGAAGTCTCTCCCGCAGCCCGCTTCAACAAGAGTCTCCCGCAGACACCGCC 429
QY 141 AsnAspLLeuMetLeuValLysMetAlaSerProValSerLLeuThrAlaValArgPro 160
DB 430 AATGACATCATCTGTGTGAAGATGGCATGCCAGTCTCATGACCTGCGCTGTGGACCC 489
QY 161 LeuThrLeuSerSerArgGlyValThrAlaGlyThrSerCysLeuLLeuSerGlyTrpGly 180
DB 490 CTCACCTCTCTCAGAGTGTGCTGCTGAGACCAAGCTGCTCATATTCGGCTGGGGC 549
QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnLLeuThrIle 200
DB 550 AACAGCTCCAGCCCGCAGTTAGCCTGCTGCACACTTCCGATGCCCAACATCACATC 609
QY 201 LLeuGlnHisGlnLysCysGlnAsnAlaTyrProGlyAsnLLeuThrAspThrMetValCys 220
DB 610 ATTTGAGCACAGAAAGTGTGAGAACGCTACCCCGGCAACATCAGACACCATGTGTGT 669
QY 221 AlaSerValGlnGlyGlyLysAspSerCysGlnGlyAspSerGlyGlyProLeuVal 240
DB 670 GCCAGGCTCAGAGAAAGGGGCAAGGACTCTCTCCAGGGGAGCTCCGGGGGCTCTGGTC 729
QY 241 CysAsnGlnSerLeuGlnGlyLLeuSerTrpGlyGlnAspProCysAlaLLeuThrArg 260
DB 720 TGTAAACAGTCTCTCAAGGCAATTAATCTCTGGGGCAGAGATCCGTTGCCATCACCCGA 789
QY 261 LysProGlyValTyrThrLysValCysLysTyrValAspTrpLLeuGlnLLeuThrMetLys 280
DB 790 AAGCTGTGTCTACAGCAAAAGTGTGCAAAATATGTGACTGTGATCCAGAGACGATGAAG 849
QY 281 AsnAsn 282
DB 850 AACCAAT 855
  
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RESULT 14
 ID AAA61763
 AC AAA61763;
 XX
 XX
 DT 23-OCT-2000 (first entry)

DE CDNA encoding human serine protease BSSP6 (hBSSP6) SEQ ID NO.1.
 KW BSSP6; serine protease; human; hBSSP6; mouse; mBSSP6; brain;
 KW diagnostic marker; antibody; transgenic animal; Alzheimer's disease;
 KW epilepsy; cancer; inflammation; infertility; pancreatitis;
 KW prostatic hypertrophy; ss.
 OS Homo sapiens.
 PN WO200031257-A1.
 XX
 XX
 PD 02-JUN-2000.
 PF 19-NOV-1999; 99WO-JP064476.
 XX
 PR 20-NOV-1998; 98UP-0347802.
 XX
 PA (FUSO) FUSO PHARM IND LTD.
 PI Uemura H, Okui A, Kominami K, Yamaguchi N, Mitsu S;
 XX
 DR WPI; 2000-40067/34.
 DR P-PSDB; AAB11712.
 XX
 PT Serine protease BSSP6, useful in detecting homologs, mutants and
 PT polymorphic variants as markers for diagnosis of Alzheimer's disease,
 PT epilepsy, cancer, inflammation, infertility and prostate hypertrophy,
 PT using blood or other tissues
 XX
 XX
 XX Claim 2; Page 67-69; 94pp; Japanese.
 CC The invention relates to novel serine proteases designated BSSP6
 CC (AAB11712-B11714), and to nucleic acids encoding them (AAA61763-A61765).
 CC The invention also relates to vectors and transformants comprising BSSP6
 CC nucleic acids; transgenic animals in which the expression level of BSSP6
 CC can be varied; and an mBSSP6 knockout mouse. The invention additionally
 CC encompasses anti-BSSP6 antibodies and methods of production of such
 CC antibodies; methods of BSSP6 detection using the antibodies, and the
 CC use of BSSP6 proteins or fragments as diagnostic markers for certain
 CC medical conditions. Nucleotides encoding BSSP6 were initially
 CC isolated in a human brain CDNA library using degenerate PCR primers
 CC (AAB61795-A61796) based on conserved regions of serine proteases. The
 CC BSSP6 serine proteases and nucleotides encoding them are useful in
 CC detecting homologues, mutants and polymorphic variants in biological
 CC samples (e.g., blood, urine, brain, prostate gland, placenta, testis
 CC and spleen) as diagnostic markers for conditions such as Alzheimer's
 CC disease, epilepsy, cancer, inflammation, infertility and prostatic
 CC hypertrophy. Sequences AAA61763 and AAA61765 represent cDNAs encoding
 CC human BSSP6 variants (hBSSP6) and sequence AAA61764 represents CDNA
 CC encoding murine BSSP6 (mBSSP6).
 XX
 XX
 SQ Sequence 1301 BP; 332 A; 387 C; 330 G; 252 T; 0 other;

Alignment Scores:
 Pred. No.: 2,76e-122 Length: 1301
 Score: 1523.00 Matches: 282
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 21 Gaps: 0

US-09-856-320A-2 (1-282) x AAA61763 (1-1301)

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QY 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAla 20
DB 113 ATGCAAGAGTTGAGTGGCTGGCGGACTGGAAGTCACTCCGGCAGAGTCTCACAGCAGCC 172
QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgLLeuGlnLeu 40
DB 173 AAGGAACCTGGGGCCGCTCTCCCTCCAGGCAATGAGATTGCAAGTTAATCTG 232
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyLeuThrArgLLeuGlyPheGlyCys 60
  
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Db      233 CTTCCTCTGGCAACAGGCGCTTGAGGGGAGAGACCAGATATCATAGGGGTTCCAGTCC 292
Qy      61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGluLysThrArgLeuLeuGly 80
Db      293 AAGCCTCACTCCAGGCGCTGGCAGGCGAGCCCTGTTGAGAGACGCGGCTACTCTGTGG 352
Qy      81 AlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTrp 100
Db      353 GCGAGCGCTATCGCCCCGAGATGGCTCCGACAGCGCCACTGCTCAAGCCCGCTAC 412
Qy      101 IleValHisLeuGluGlnHisAsnLeuGlnLysGluGluGlyCysGluGlnThrArgTrp 120
Db      413 ATAGTTCACTCGGGGAGACCAACCTCCAGAGAGAGAGGGCTGTAGACAGACCGGACA 472
Qy      121 AlaThrGlnSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
Db      473 GGCACGTAGTCTCTCCCGCACCCCGGCTTCAACAACAGCGCTCCCAACAAGACCGCC 532
Qy      141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
Db      533 ATATGACATCATCTGATGAGATGAGATGCGATGCTCCATCATCCTGGGCTGTGCGACCC 592
Qy      161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuLysSerGlyTrpGly 180
Db      593 CTCACCCCTCTCTCAAGCTGTGTCACTGCTGGCACCAAGCTGCTCATTTCCGGCTGGGC 652
Qy      181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
Db      653 AGCAGCGTCAGGCCCGCAGTTACGCTGCTGCTCACACCTTCGATGCGCCAAACATCACATC 712
Qy      201 ILeGluHisGlnLysGlnLysAlaAlaTrpProGlyAsnIleThrAspThrMetValCys 220
Db      713 ATTTGAGACCAAGAGTGAAGAACGCTTACCCCGGACATCATCAGACACCATGGTGT 772
Qy      221 AlaSerValGlnGluGlyLysAspSerCysGlnGlyAspSerGlyLysProLeuVal 240
Db      773 GCCAGCGTCCAGGAAGGGGCAAGACCTCTCCAGCGTCACTCCGGGGCCCTCTGGTC 832
Qy      241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
Db      833 TGTAAACAGACTCTCTCAAGGCAATTATCTCTGGGGGCGAGATCCGCTCGATCACCCGA 892
Qy      261 LysProGlyValTyrThrLysValCysLysTyrValAspTrpIleGlnIleThrMetLys 280
Db      893 AAGCCTGGTGTACACGAAGCTTGCATAATATGTGACTGATCCAGAGACGATGAAG 952
Qy      281 AsnAsn 282
Db      953 AACAAAT 958

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RESULT 15

AAZ30222 standard; cDNA; 1314 BP.

AAZ30222;

11-FEB-2000 (first entry)

cDNA encoding a human prostate-associated serum protease (PRASP).

Human; prostate-associated serum protease; PRASP; neuropsin; PSA; Incyte clone 2723646; reproductive disorder; cancer; abnormal prolactin production; infertility; tubal disease; ovulatory defect; endometriosis; polycystic ovary syndrome; autoimmune disorder; ectopic pregnancy; breast cancer; abnormal spermatogenesis; testicular cancer; adenocarcinoma; leukemia; lymphoma; melanoma; myeloma; sarcoma; teratocarcinoma; ss.

Homo sapiens.

Key Location/Qualifiers
CDS 128..976
FT /tag= a
FT

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FT      FT      /product= "prostate-associated serum protease"
FT      FT      /tag= 146..181
FT      FT      /tag= b
FT      FT      /note= "these nucleotides are separately claimed
FT      FT      under claim 10"
FT      FT      misc_feature
FT      FT      344..382
FT      FT      /tag= c
FT      FT      /note= "these nucleotides are separately claimed
FT      FT      under claim 10"
FT      FT      misc_feature
FT      FT      551..589
FT      FT      /tag= d
FT      FT      /note= "these nucleotides are separately claimed
FT      FT      under claim 10"
XX      XX      WO9941387-A2.
XX      XX      19-AUG-1999.
XX      XX      05-FEB-1999; 99WO-US02571.
XX      XX      17-FEB-1998; 98US-0025059.
XX      XX      (INCY-) INCYTE PHARM INC.
XX      XX      Tang YT, Corley NC, Guegler KJ;
XX      XX      WPI; 2000-012993/01.
XX      XX      P-PSDB; AAY43636.
XX      XX      New prostate-associated serum protease and polynucleotides which
XX      XX      identify and encode PRASP, useful for treating reproductive disorders
XX      XX      and cancer.
XX      XX      Claim 7; Fig 1A-D; 67pp; English.
XX      XX
XX      XX      The present sequence encodes a human prostate-associated serum protease
XX      XX      (PRASP). The protein shows homology to neuropsin, a brain-specific
XX      XX      protease in mice, and PSA, a prostate-specific protease in humans.
XX      XX      Nucleic acids encoding PRASP were first identified in Incyte clone
XX      XX      2723646 from the lung tumour cDNA library. Pharmaceutical compositions
XX      XX      containing PRASP, or antibodies to PRASP, and mimetics, agonists,
XX      XX      antagonists or inhibitors of PRASP, are used for treating or preventing
XX      XX      a reproductive disorder or cancer. Examples of reproductive disorder
XX      XX      include, abnormal prolactin production, infertility, tubal disease,
XX      XX      ovulatory defects, endometriosis, polycystic ovary syndrome, autoimmune
XX      XX      disorders, ectopic pregnancy, breast cancer, abnormal spermatogenesis
XX      XX      and testicular cancer. Examples of cancers which may be treated or
XX      XX      prevented include adenocarcinoma, leukemia, lymphoma, melanoma, myeloma,
XX      XX      sarcoma, teratocarcinoma, and cancers of the adrenal gland, bladder,
XX      XX      bone, bone marrow, brain, breast, cervix, penis, prostate, salivary
XX      XX      glands, skin, spleen, testis, thymus, thyroid and uterus. A vector
XX      XX      capable of expressing PRASP or an agonist which modulates the activity of
XX      XX      PRASP may be administered to treat or prevent a reproductive disorder or
XX      XX      cancer.
XX      XX
XX      XX      Sequence 1314 BP; 320 A; 400 C; 337 G; 257 T; 0 other.
XX      XX
XX      XX      Alignment Scores:
XX      XX      Pred. No.: 2,79e-122 Length: 1314
XX      XX      Score: 1523.00 Matches: 282
XX      XX      Percent Similarity: 100.00% Conservative: 0
XX      XX      Best Local Similarity: 100.00% Mismatches: 0
XX      XX      Query Match: 100.00% Indels: 0
XX      XX      DB: 21 Gaps: 0
XX      XX
XX      XX      US-09-856-320A-2 (1-282) x AAZ30222 (1-1314)
Qy      1 MetGlnArgLeuAlaGTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaAla 20
Db      128 ATGCGAGAGTGGAGTGGCTCGGAGATGAGTCAAGTATCTGCGACAGGCTCATCAGCACCC 187
Qy      21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleLeu 40

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Db 188 AAGGAAGCTGGGGCCGCTCTCCCTCCAGCCATGAGATTCGCAATTATCTG 247
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyLeuThrArgIleIleValGlyPheGlyCys 60
Db 248 CTGGCTCTGGCAACAGGGCTTTAGGGGAGAGACAGGATCATCAAGGGTTGAGTGC 307
QY 61 LysProHisSerGlnProTTPGlnAlaAlaLeuPheGlnLysThrArgLeuLeuGly 80
Db 308 AAGCCTCAGCTCCAGCCCTGGCAGCAGCCCTGTTCAGAAAGACGGCGCTACTGTGGG 367
QY 81 AlaThrLeuIleAlaProArgTTPLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
Db 368 GCGAGCCTCATCGCCCCAGATGCTCTGACAGAGCCCATCGCTCAAGCCCCGCTAC 427
QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlyGlyGlnThrArgThr 120
Db 428 ATAGTTCACCTGGGAGACACAACTCCAGAGAGAGAGGGCTGTGAGACAGACCGGACA 487
QY 121 AlaThrGlnSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
Db 488 GCGACTGAGTCTTCCCGCCAGCTCCCAACACAGCCTCCCAACAAAGACACCGC 547
QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTTPAlaValArgPro 160
Db 548 AATGACATCATGCTGTGAAGATGCGATCGCAGTCTCCATCATCGCTGGCTGTGCGACCC 607
QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTTPGly 180
Db 608 CTCACCCCTCTCTCAGCGTGTGTGCTGCTGGCAGCAGCTGCTCATTTCCGGCTGGGGC 667
QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
Db 668 AGCAGCTCCAGCCCCAGTTAGCGCTGCTCAGACCTTGCGATGCGCCAAACATCACCATC 727
QY 201 IleGlnHisGlnLysCysGlnAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220
Db 728 ATTGAGCACACAGAGTGTGAAGACGCTTACCCCGGCACATCACACATCATGTGTGT 787
QY 221 AlaSerValGlnGlyGlyLysAspSerCysGlnGlyAspSerGlyLysProLeuVal 240
Db 788 GCGAGCGTGCAGAGAGGGGCAAGAGCTCTGCGAGGTGACTCCGGGGGCCCTCTGTGTC 847
QY 241 CysAsnGlnSerLeuGlnGlyIleIleSerTTPGlyGlnAspProCysAlaIleThrArg 260
Db 848 TGTAAACAGTCTCTCAAGCATTTATCTCTGGGGCAGAGATCCGTTGCGATCACCGCA 907
QY 261 LysProGlyValTyrThrLysValCysLysTyrValAspTTPIleGlnGlnThrMetLys 280
Db 908 AAGCCTGGTGTCTACAGAAAGTCTGCATAATATGTGACTGTGATCCAGAGACGATGAAG 967
QY 281 AsnAsn 282
Db 968 AACAAAT 973

Search completed: October 23, 2003, 15:58:06
Job time : 323.145 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: October 23, 2003, 15:49:25 ; Search time 309.593 Seconds

(without alignments)
2442.781 Million cell updates/sec

Title: US-09-856-320A-2

Perfect score: 1523

Sequence: 1 MORLRWLRDMKSSGRGLTAA.....GYTVKVKYVDWIQETMKKN 282

Scoring table:

	BLOSUM62
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delpop 6.0 , Delpext 7.0	

Searched: 1792395 seqs, 1340900451 residues

Total number of hits satisfying chosen parameters: 3584790

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n -DEV=xlh
-Q=/cg2_1/USPTO_spool/US09856320/runat_22102003_121415_25716/app_query.fasta_1.846
-DB=PubMed_Application_NA -QMT=fastcap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPEL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=biosum62
-TRANS=human40.cdi -LIST=45 -LOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09856320 @CGN 1.1 347 @runat_22102003_121415_25716
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NBG_SCORES=0 -WAIT -DSPELACK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FCAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:*

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2:	/cg2_6/ptodata/1/pubna/PCT_NEW_PUB.seq:*
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17:	/cg2_6/ptodata/1/pubna/US60_PUBCOMB.seq:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1523	100.0	1186	14	US-10-205-823-211 Sequence 211, App

2	1523	100.0	1204	11	US-09-946-374-169 Sequence 169, App
3	1523	100.0	1204	12	US-10-015-387A-169 Sequence 169, App
4	1523	100.0	1204	12	US-10-137-870-505 Sequence 505, App
5	1523	100.0	1204	12	US-10-140-018-505 Sequence 505, App
6	1523	100.0	1204	12	US-10-140-021-505 Sequence 505, App
7	1523	100.0	1204	12	US-10-140-274-505 Sequence 505, App
8	1523	100.0	1204	12	US-10-140-471-505 Sequence 505, App
9	1523	100.0	1204	12	US-10-140-807-505 Sequence 505, App
10	1523	100.0	1204	12	US-10-140-922-505 Sequence 505, App
11	1523	100.0	1204	12	US-10-140-924-505 Sequence 505, App
12	1523	100.0	1204	12	US-10-140-926-505 Sequence 505, App
13	1523	100.0	1204	12	US-10-141-658-505 Sequence 505, App
14	1523	100.0	1204	12	US-10-141-702-505 Sequence 505, App
15	1523	100.0	1204	12	US-10-141-704-505 Sequence 505, App
16	1523	100.0	1204	12	US-10-142-431-505 Sequence 505, App
17	1523	100.0	1204	12	US-10-142-432-505 Sequence 505, App
18	1523	100.0	1204	12	US-10-142-767-505 Sequence 505, App
19	1523	100.0	1204	12	US-10-143-033-505 Sequence 505, App
20	1523	100.0	1204	12	US-10-144-994-505 Sequence 505, App
21	1523	100.0	1204	12	US-10-145-628-505 Sequence 505, App
22	1523	100.0	1204	12	US-10-145-631-505 Sequence 505, App
23	1523	100.0	1204	12	US-10-145-633-505 Sequence 505, App
24	1523	100.0	1204	12	US-10-145-746-505 Sequence 505, App
25	1523	100.0	1204	12	US-10-145-748-505 Sequence 505, App
26	1523	100.0	1204	12	US-10-145-823-505 Sequence 505, App
27	1523	100.0	1204	12	US-10-145-826-505 Sequence 505, App
28	1523	100.0	1204	12	US-10-145-870-505 Sequence 505, App
29	1523	100.0	1204	12	US-10-145-876-505 Sequence 505, App
30	1523	100.0	1204	12	US-10-145-959-505 Sequence 505, App
31	1523	100.0	1204	12	US-10-146-724-505 Sequence 505, App
32	1523	100.0	1204	12	US-10-146-725-505 Sequence 505, App
33	1523	100.0	1204	12	US-10-146-795-505 Sequence 505, App
34	1523	100.0	1204	12	US-10-147-495-505 Sequence 505, App
35	1523	100.0	1204	12	US-10-147-501-505 Sequence 505, App
36	1523	100.0	1204	12	US-10-147-504-505 Sequence 505, App
37	1523	100.0	1204	12	US-10-147-506-505 Sequence 505, App
38	1523	100.0	1204	12	US-10-147-509-505 Sequence 505, App
39	1523	100.0	1204	12	US-10-147-510-505 Sequence 505, App
40	1523	100.0	1204	12	US-10-147-511-505 Sequence 505, App
41	1523	100.0	1204	12	US-10-147-529-505 Sequence 505, App
42	1523	100.0	1204	12	US-10-152-397-505 Sequence 505, App
43	1523	100.0	1204	12	US-10-153-586-505 Sequence 505, App
44	1523	100.0	1204	12	US-10-158-783-505 Sequence 505, App
45	1523	100.0	1204	12	US-10-158-786-505 Sequence 505, App

ALIGNMENTS

RESULT 1
US-10-205-823-211
; Sequence 211, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gotbacheva, Bella
; APPLICANT: Hoerscher, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Womsey, Angela M.
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356

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; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FASTSeq for Windows Version 4.0
; SEQ ID NO: 211
; LENGTH: 1186
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-823-211

Alignment Scores:
Pred. No.: 5,086-162 Length: 1186
Score: 1523.00 Matches: 282
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-856-320A-2 (1-282) x US-10-205-823-211 (1-1186)

QY 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaAla 20
DB 26 ATGCAGAGGTTGAGGTGGCTGGCGGACGTGAGTATCCGGACAGAGTCTCACACAGCC 85
QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgLLeuGlnLeuLeu 40
DB 86 AAGGAACCTGGGGCCCGCTCTCCCGCCCGGACGATGAGGATTCGAGTAATCCCG 145
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyGlnTrpArgLeuLeuLysGlyPheGlyGly 60
DB 146 CTGGCTCTGGCAACAGGGCTTGTAGGGGAGAGACAGGATCATCAGGGGTTCCAGTGC 205
QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlyLysThrArgLeuLeuGly 80
DB 206 AAGCTCTACCTCCACCCCTGGGACGAGCCCTGTTGAGAAACCGGCTACTCTGTGG 265
QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTrp 100
DB 266 GCGACGCTCATGCCCCCAGATGGCTCTTGACAGACGCCACTGCTCAAGCCCCGCTAC 325
QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlyGlyCysGlyGlnThrArgThr 120
DB 326 ATAGTTCACTGGGGACAGACAACTCCAGAGAGAGAGGGCTGTGAGAGACCCGGACA 385
QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
DB 386 GCCACTGAGTCTCTCCACCCCGCTTCAACAAACAGCTCTCCCAACAAACACACCGC 445
QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTyrAlaValArgPro 160
DB 446 AATGACATCATCTCTGTGAAGATGCATGCCAGTCTCCATCACTGGGCTGTGGACCC 505
QY 161 LeuThrLysSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
DB 506 CTCACCTCTCTCTACGCTGTCTACTGCTGGCACACAGTGTCTATTTCCGGCTGGGG 565
QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
DB 566 AGCAGGTCACAGCCCCCAGTTACGCTGCTCCACACTTGCATGCGCAACATCACCATC 625
QY 201 IleGlnHisGlnLysCysGlnAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220
DB 626 ATTGACACCCAGAAAGTGTGAGAGACGCTTACCCCGGCAACATACAGACACCATGGTGT 685
QY 221 AlaSerValGlnGlyGlyLysAspSerCysGlnGlyAspSerGlyGlyProLeuVal 240
DB 686 GCCACGTCGAGAGAGGGGGGCAAGGACTCTCTCCAGGGGTAAGTCCGGGGGCCCTCTGTC 745
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QY 241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyLysAspProCysAlaIleThrArg 260
DB 746 TGTAAACGATCTCTTCAAGGAGATTATCTCTGGGAGCAGAGATCCGTGCGCATCACCCGA 805
QY 261 LysProGlyValIleThrLysValCysLysTrpValAspTrpIleGlnGlnThrMetLys 280
DB 806 AAGCTGTGTCTTACACGAAAGTCTGCAAAATATGTGACCTGATCCAGACACATGAG 865
QY 281 AsnAsn 282
DB 866 AACAAAT 871

RESULT 2
US-09-946-374-169
; Sequence 169, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/946,374
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
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; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
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; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
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PRIOR APPLICATION NUMBER:	60/099808
PRIOR FILING DATE:	1998-09-10
PRIOR APPLICATION NUMBER:	60/099812
PRIOR FILING DATE:	1998-09-10
PRIOR APPLICATION NUMBER:	60/099815
PRIOR FILING DATE:	1998-09-10
PRIOR APPLICATION NUMBER:	60/099816
PRIOR FILING DATE:	1998-09-10
PRIOR APPLICATION NUMBER:	60/100355
PRIOR FILING DATE:	1998-09-15
PRIOR APPLICATION NUMBER:	60/100388
PRIOR FILING DATE:	1998-09-15
PRIOR APPLICATION NUMBER:	60/100390
PRIOR FILING DATE:	1998-09-15
PRIOR APPLICATION NUMBER:	60/100584
PRIOR FILING DATE:	1998-09-16
PRIOR APPLICATION NUMBER:	60/100627
PRIOR FILING DATE:	1998-09-16
PRIOR APPLICATION NUMBER:	60/100641
PRIOR FILING DATE:	1998-09-16
PRIOR APPLICATION NUMBER:	60/100649
PRIOR FILING DATE:	1998-09-16
PRIOR APPLICATION NUMBER:	60/100663
PRIOR FILING DATE:	1998-09-17
PRIOR APPLICATION NUMBER:	60/100684
PRIOR FILING DATE:	1998-09-17
PRIOR APPLICATION NUMBER:	60/100710
PRIOR FILING DATE:	1998-09-17
PRIOR APPLICATION NUMBER:	60/100711
PRIOR FILING DATE:	1998-09-17
PRIOR APPLICATION NUMBER:	60/100848
PRIOR FILING DATE:	1998-09-18
PRIOR APPLICATION NUMBER:	60/100849
PRIOR FILING DATE:	1998-09-18
PRIOR APPLICATION NUMBER:	60/100919
PRIOR FILING DATE:	1998-09-17
PRIOR APPLICATION NUMBER:	60/100930
PRIOR FILING DATE:	1998-09-17
PRIOR APPLICATION NUMBER:	60/101014
PRIOR FILING DATE:	1998-09-18
PRIOR APPLICATION NUMBER:	60/101056
PRIOR FILING DATE:	1998-09-18
PRIOR APPLICATION NUMBER:	60/101071
PRIOR FILING DATE:	1998-09-18
PRIOR APPLICATION NUMBER:	60/101279
PRIOR FILING DATE:	1998-09-22
PRIOR APPLICATION NUMBER:	60/101471
PRIOR FILING DATE:	1998-09-23
PRIOR APPLICATION NUMBER:	60/101472
PRIOR FILING DATE:	1998-09-23
PRIOR APPLICATION NUMBER:	60/101474
PRIOR FILING DATE:	1998-09-23
PRIOR APPLICATION NUMBER:	60/101475
PRIOR FILING DATE:	1998-09-23
PRIOR APPLICATION NUMBER:	60/101476
PRIOR FILING DATE:	1998-09-23
PRIOR APPLICATION NUMBER:	60/101477
PRIOR FILING DATE:	1998-09-23
PRIOR APPLICATION NUMBER:	60/101479
PRIOR FILING DATE:	1998-09-23
PRIOR APPLICATION NUMBER:	60/101738
PRIOR FILING DATE:	1998-09-24
PRIOR APPLICATION NUMBER:	60/101741
PRIOR FILING DATE:	1998-09-24
PRIOR APPLICATION NUMBER:	60/101743
PRIOR FILING DATE:	1998-09-24
PRIOR APPLICATION NUMBER:	60/101915
PRIOR FILING DATE:	1998-09-24
PRIOR APPLICATION NUMBER:	60/101916

PRIOR FILING DATE: 1998-09-24	PRIOR APPLICATION NUMBER: 60/102207
PRIOR FILING DATE: 1998-09-29	PRIOR APPLICATION NUMBER: 60/102240
PRIOR FILING DATE: 1998-09-29	PRIOR APPLICATION NUMBER: 60/102307
PRIOR FILING DATE: 1998-09-29	PRIOR APPLICATION NUMBER: 60/102330
PRIOR FILING DATE: 1998-09-29	PRIOR APPLICATION NUMBER: 60/102331
PRIOR FILING DATE: 1998-09-29	PRIOR APPLICATION NUMBER: 60/102484
PRIOR FILING DATE: 1998-09-30	PRIOR APPLICATION NUMBER: 60/102487
PRIOR FILING DATE: 1998-09-30	PRIOR APPLICATION NUMBER: 60/102570
PRIOR FILING DATE: 1998-09-30	PRIOR APPLICATION NUMBER: 60/102571
PRIOR FILING DATE: 1998-09-30	PRIOR APPLICATION NUMBER: 60/102684
PRIOR FILING DATE: 1998-10-01	PRIOR APPLICATION NUMBER: 60/102687
PRIOR FILING DATE: 1998-10-01	PRIOR APPLICATION NUMBER: 60/102688
PRIOR FILING DATE: 1998-10-02	PRIOR APPLICATION NUMBER: 60/102955
PRIOR FILING DATE: 1998-10-02	PRIOR APPLICATION NUMBER: 60/103258
PRIOR FILING DATE: 1998-10-06	PRIOR APPLICATION NUMBER: 60/103314
PRIOR FILING DATE: 1998-10-07	PRIOR APPLICATION NUMBER: 60/103315
PRIOR FILING DATE: 1998-10-07	PRIOR APPLICATION NUMBER: 60/103328
PRIOR FILING DATE: 1998-10-07	PRIOR APPLICATION NUMBER: 60/103355
PRIOR FILING DATE: 1998-10-07	PRIOR APPLICATION NUMBER: 60/103449
PRIOR FILING DATE: 1998-10-07	PRIOR APPLICATION NUMBER: 60/103396
PRIOR FILING DATE: 1998-10-07	PRIOR APPLICATION NUMBER: 60/103401
PRIOR FILING DATE: 1998-10-07	PRIOR APPLICATION NUMBER: 60/103459
PRIOR FILING DATE: 1998-10-06	PRIOR APPLICATION NUMBER: 60/103633
PRIOR FILING DATE: 1998-10-08	PRIOR APPLICATION NUMBER: 60/103678
PRIOR FILING DATE: 1998-10-08	PRIOR APPLICATION NUMBER: 60/103679
PRIOR FILING DATE: 1998-10-08	PRIOR APPLICATION NUMBER: 60/103711
PRIOR FILING DATE: 1998-10-08	PRIOR APPLICATION NUMBER: 60/104257
PRIOR FILING DATE: 1998-10-14	PRIOR APPLICATION NUMBER: 60/104967
PRIOR FILING DATE: 1998-10-20	PRIOR APPLICATION NUMBER: 60/105000
PRIOR FILING DATE: 1998-10-20	PRIOR APPLICATION NUMBER: 60/105002
PRIOR FILING DATE: 1998-10-20	PRIOR APPLICATION NUMBER: 60/105104
PRIOR FILING DATE: 1998-10-21	PRIOR APPLICATION NUMBER: 60/105169
PRIOR FILING DATE: 1998-10-22	PRIOR APPLICATION NUMBER: 60/105266
PRIOR FILING DATE: 1998-10-22	PRIOR APPLICATION NUMBER: 60/105693
PRIOR FILING DATE: 1998-10-26	PRIOR APPLICATION NUMBER: 60/105654
PRIOR FILING DATE: 1998-10-26	PRIOR APPLICATION NUMBER: 60/105807

Alignment Scores:		
Pred. No.:	5.19e-162	Length: 1204
Score:	1523.00	Matches: 282
Percent Similarity:	100.00%	Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 11 Gaps: 0

US-09-856-320A-2 (1-282) x US-09-946-374-169 (1-1204)

```

QY 1 MetGlnArgLeuArgTyrLeuArgAspTyrPlySerSerGlyValArgGlyLeuThrAla 20
DB 10 ATGCAGAGGTGAGGTGGCTGGCGGCTGGAGTCAATCGGCGAGAGGTCTCACAGCAGCC 69
QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeu 40
DB 70 AAGGAACCTGGGGCCGCTCTCTCCCTCCAGCCATAGAGATTCTGCAGTTAATCTTG 129
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyIuThrArgIleIleLysGlyPheGlyCys 60
DB 130 CTTCGCTCTGGCAACAGGGCTTGGAGGGGAGAGACAGGATCATCAGGGGTTCCAGTGC 189
QY 61 LysProHisSerGlnProTyrGlnAlaAlaLeuPheGlyIuThrArgLeuLeuGly 80
DB 190 AAGCTCATCTCCAGCCCTGGCGAGCGACGCTGTTCGAGAAAGACCGGCTACTCTGTGG 249
QY 81 AlaThrLeuIleAlaProArgTyrLeuThrAlaAlaHisCysLeuLysProArgTyr 100
DB 250 GCGAGCTCATCGCCCCGAGATGGCTCTTCGACAGAGCCCTGCTCAAGCCCGCTAC 309
QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlnGlyCysGluGlnThrArgThr 120
DB 310 AATAGTTACACTGGGGAGCACAACCTCCAGAGAGAGAGGGTGTGAGCAGACCCGGACA 369
QY 121 AlaThrGluSerPheProHisSerProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
DB 370 GCCACTGACTCTTCCGCCACCCCGGCTTCAACACAGCTCCCAACAAAGACCAACCC 429
QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTyrAlaValArgPro 160
DB 430 AATGACATATGCTGTGAAGATGGCATGCGAGTTCATCATCCTGGGCTGTGGAGCC 489
QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTyrGly 180
DB 490 CTCACCTCTCTCAAGCTGTGTCACTGTGGCACAGCTGCTCATTTCCGGCTGGGGC 549
QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
DB 550 AGCAGCTCCAGCCCCAGTTACGCTGCTGCACCTGCGATGCGCCCAACATCAACATC 609
QY 201 IleGluHisGlnLysCysGlnAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220
DB 610 ATTGAGCACCAAGATGTGAGAACGCTTACCCGGCAGCATCAAGACCCATGTGTGT 669
QY 221 AlaSerValGlnGluGlyLysLysAspSerCysGlnGlyAspSerGlyCysProLeuVal 240
DB 670 GCCACGTCGACAGAGGGGCAAGGACTCTCTCCAGGGTGACTCCGGGGCCCTCTGGTC 729
QY 241 CysAsnGlnSerLeuGlnGlyIleIleSerTyrGlyGlnAspProCysAlaIleThrArg 260
DB 730 TGTAACTCACTCTTCAAGGCAATTAATCTCTGGGGCAGAGATCCGTGTGCGATCAACCGA 789
QY 261 LysProGlyValIleThrLysValCysLysTyrValAspTyrIleGlnGlnThrMetLys 280
DB 790 AAGCTGTGTCTTACACGAAAGTCTGCATAATATGTGACTGATCCAGAGACGATGANG 849
QY 281 AsnAsn 282
DB 850 AACCAAT 855

```

RESULT 3

US-10-015-387A-169
 ; Sequence 169, Application US/10015387A
 ; Publication No. US20030135034A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David

```

; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C54
; CURRENT APPLICATION NUMBER: US/10/015,387A
; CURRENT FILING DATE: 2001-12-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 169
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-015-387A-169

Alignment Scores:
Pred. No.: 5,19e-162 Length: 1204
Score: 1523.00 Matches: 282
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-856-320A-2 (1-282) x US-10-015-387A-169 (1-1204)
QY 1 MetGlnArgLeuArgTyrLeuArgAspTyrPlySerSerGlyValArgGlyLeuThrAla 20
DB 10 ATGCAGAGGTGAGGTGGCTGGCGGCTGGAGTCAATCGGCGAGAGGTCTCACAGCAGCC 69
QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeu 40
DB 70 AAGGAACCTGGGGCCGCTCTCTCCCTCCAGCCATAGAGATTCTGCAGTTAATCTTG 129
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyIuThrArgIleIleLysGlyPheGlyCys 60
DB 130 CTTCGCTCTGGCAACAGGGCTTGGAGGGGAGAGACAGGATCATCAGGGGTTCCAGTGC 189
QY 61 LysProHisSerGlnProTyrGlnAlaAlaLeuPheGlyIuThrArgLeuLeuGly 80
DB 190 AAGCTCATCTCCAGCCCTGGCGAGCGACGCTGTTCGAGAAAGACCGGCTACTCTGTGG 249
QY 81 AlaThrLeuIleAlaProArgTyrLeuThrAlaAlaHisCysLeuLysProArgTyr 100
DB 250 GCGAGCTCATCGCCCCGAGATGGCTCTTCGACAGAGCCCTGCTCAAGCCCGCTAC 309
QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlnGlyCysGluGlnThrArgThr 120
DB 310 AATAGTTACACTGGGGAGCACAACCTCCAGAGAGAGAGGGTGTGAGCAGACCCGGACA 369
QY 121 AlaThrGluSerPheProHisSerProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
DB 370 GCCACTGACTCTTCCCGCACCCCGGCTTCAACAAAGCTCCCAACAAAGACCAACCC 429
QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTyrAlaValArgPro 160
DB 430 AATGACATATGCTGTGAAGATGGCATGCGAGTTCATCATCCTGGGCTGTGGAGCC 489
QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTyrGly 180
DB 490 CTCACCTCTCTCAAGCTGTGTCACTGTGGCACAGCTGCTCATTTCCGGCTGGGGC 549
QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200

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Db 550 AGCAGCTCCAGCCCGCATTTACGCTGCTGCATCACCTTGAGATGGCCAAATCACCATT 609

QY 201 IIEGLIHISGLINLYSCYSGIUASNAIATYTPROGIIYASNIIEThrsphrmetValCys 220

Db 610 ATTGACACACAGAAAGTGTGAGAAAGCTTACCGGCAACCTCACAACACCATGAGTGT 669

QY 221 AIAseValGIngluGlyGlyAspSerCysGInglYAspSerGlyGlyProLeuVal 240

Db 670 GCCAGGCTGCAGAGAGGGGCAAGACTCTCTGCCAGGGTACTCCGGGGCCCTCTGTGTC 729

QY 241 CysAsnGInserLeuGInglYIleIleSerTPGIIYGInAspProCysAlaIleThrsArg 260

Db 730 TGTAAACAGCTCTCTTAAGGCAATTATCTCTGGGGCCAGGATCCGTGCGATCACCCGA 789

QY 261 LysProGIIYValIYThrIleThrsValCysLysTYrValAspTropIleGIngluThrMetLys 280

Db 790 AACCCCTGGTGTCTTACAGAAAGTGTCAATATATGTGACTGATCCAGAGAGATGAAG 849

QY 281 AsnAsn 282

Db 850 AACAAAT 855

RESULT 4

US-10-137-870-505

Sequence 505, Application US/10137870

Publication No. US2003013883A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen

APPLICANT: DeForge, Laura

APPLICANT: Desnoyers, Luc

APPLICANT: Filvaroff, Ellen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Sherwood, Steven

APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3330R1C155

CURRENT APPLICATION NUMBER: US/10/137,870

CURRENT FILING DATE: 2002-05-03

Prior Application removed - See Palm or File Wrapper

NUMBER OF SEQ ID NOS: 550

SEQ ID NO 505

LENGTH: 1204

TYPE: DNA

ORGANISM: Homo Sapien

US-10-137-870-505

Alignment Scores:

Pred. No.: 5,19e-162 Length: 1204

Score: 1523.00 Matches: 282

Percent Similarity: 100.00% Conservatave: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 12 Gaps: 0

US-09-856-320A-2 (1-282) x US-10-137-870-505 (1-1204)

QY 1 MetGInARLeuARITrpleuARgAspTrpLysSerSerGIIYArgGIIYleuThraAla 20

Db 10 ATGCAAGAGGTGAGGTGCTGCGGAGCTGGAAGTATCGGAGAGAGGTCTCACAGAGCC 69

QY 21 LysGluProGIIYAlaIARSerSerProLeuGInAlaMetArgIleuGInleuIleu 40

Db 70 AAGGAACCTGGGGCCCGCTCTCCCCCTCCAGGCCATGAGGATTCCTGAGTTAATCTCG 129

QY 41 LeuAlaLeuAlaThrGIIYleuValGlyGlyIuThrsArgIleIleLysGlyPheGlyCys 60

Db 130 CTYGTCTGGCAACAGGGCTTGTAGGGGAGAGACCATGATCATCAAGGGGTTCGATGC 189

QY 61 LysProHisSerGIIYProTPGIIYAlaIleAlaLeuPheGIIYLYsThrsArgLeuLeuCysGly 80

Db 190 AAGCTCTACTCCCAAGCCCTGGGACAGGAGCCCTGTTGAGAAACCGGGCTACTCTGTGG 249

QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThraIleAlaHisCysLeuLysProArgTYr 100

Db 250 GCGAGCTCATGCGCCCGCATGAGTGGCTCTGACAGAGAGCCACTGCTCAAGCCCGCTAC 309

QY 101 IIEValHisLeuGIIYGInHisAsnLeuGInLYsGluGluGlyCysGluGInThrsArgTr 120

Db 310 ATAGTTCACTGGGGACAGCAACCTCCAGAAAGGAGAGGGTGTGTAGAGACCCCGACA 369

QY 121 AlaThrGInSerPheProHisProGIIYPheAsnAsnSerLeuProAsnLysAspHisArg 140

Db 370 GCCACTGAGTCTCTTCCCCCAGCCCGCTTCAACACAGCTCTCCCAACAAAGCACCCG 429

QY 141 AsnAspIleMetLeuValIleLysMetAlaSerProValSerIleThrsTrpAlaValArgPro 160

Db 430 AATGACATCATGCTGTGTGAAGATGGCATGCGCAGTCTCATCATCCGTGGGCTGTGGAGCC 489

QY 161 LeuThrsLeuSerSerArgCysValThrsArgIYThrsCysLeuIleSerGIIYTrpGly 180

Db 490 CTCACCCCTCTCTCAAGCTGTGTCTCACTGCTGACACAGCTGCTCATATTCGCGTGGG 549

QY 181 SerThrsSerProGIIYleuArgLeuProHisThrsTrpLeuArgCysAlaAsnIleThrs 200

Db 550 AGCAGCTCAGCCCGCATGTACGCTGCTGCCTCACCTTGCGATGGCCAAATCCACCATC 609

QY 201 IIEGLIHISGLINLYSCYSGIUASNAIATYTPROGIIYASNIIEThrsphrmetValCys 220

Db 610 ATTGACACACAGAAAGTGTGAGAAAGCTTACCGGCAACATCACAAGACCATGAGTGT 669

QY 221 AIAseValGIngluGlyGlyAspSerCysGInglYAspSerGlyGlyProLeuVal 240

Db 670 GCCAGGCTGCAGAGAGGGGCAAGACTCTCTGCCAGGGTACTCCGGGGCCCTCTGTGTC 729

QY 241 CysAsnGInserLeuGInglYIleIleSerTPGIIYGInAspProCysAlaIleThrsArg 260

Db 730 TGTAAACAGCTCTCTTAAGGCAATTATCTCTGGGGCCAGGATCCGTGCGATCACCCGA 789

QY 261 LysProGIIYValIYThrIleThrsValCysLysTYrValAspTropIleGIngluThrMetLys 280

Db 790 AACCCCTGGTGTCTTACAGAAAGTGTCAATATATGTGACTGATCCAGAGAGATGAAG 849

QY 281 AsnAsn 282

Db 850 AACAAAT 855

RESULT 5

US-10-140-018-505

Sequence 505, Application US/10140018

Publication No. US2003013885A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen

APPLICANT: DeForge, Laura

APPLICANT: Desnoyers, Luc

APPLICANT: Filvaroff, Ellen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Sherwood, Steven

APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

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; APPLICANT: Matanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C158
; CURRENT APPLICATION NUMBER: US/10/140,018
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-140-018-505

Alignment Scores:
Pred. No.: 5,19e-162 Length: 1204
Score: 1523.00 Matches: 282
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-856-320A-2 (1-282) x US-10-140-018-505 (1-1204)

Qy 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaAla 20
Db 10 ATGCAGAGGTTCAGGTGCTGGCGGAGCATGAGATCATCGGAGAGTCTCACAGCAGC 69
Qy 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgGlyLeuGlnLeu 40
Db 70 AAGGAACCTGGGGCCGCTCTCCCTCCAGGCGCATGAGATTCAGTTAATCTCG 129
Qy 41 LeuAlaLeuAlaThrGlyLeuValGlyGluThrArgGlyLeuLysGlyPheGluCys 60
Db 130 CTGCTCTGGCAGACGGGCTTGTAGGGGAGAGACAGGATATCAAGGGGTTCAAGTGC 189
Qy 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGluLysThrArgLeuLysGly 80
Db 190 AAGCTCACTCCAGCCCTGGGAGGAGCCCTGTTGAGAAAGACCGGCTACTGTGG 249
Qy 81 AlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTr 100
Db 250 GCGAGCTCATCGCCCCAGAGGCTCTGACAGAGCCCACTGCTCAAGCCCGCTAC 309
Qy 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlnGlyCysGluGlnThr 120
Db 310 ATAGTTCACTTGGGGCAGACCACTCCAGAAAGAGAGGGCTGTGAGCAGACCCGGA 369
Qy 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
Db 370 GCCACTGAGTCTCTCCGCCACCCCGGCTTCAACACAGGCTCCCAACAAAGACCAAC 429
Qy 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTyrAlaValArgPro 160
Db 430 AATGACATCATGCTGTGAAGATGGCATCGCCAGTCTCATCACTGGCGTGTGGACCC 489
Qy 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTyrGly 180
Db 490 CTCACCTCTCTCTCAGCTGTGTCTACTGTGACCACTGCTCATATTCGGGCTGGGG 549
Qy 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
Db 550 AGCAGCTCAGGCCCCAGTTAGCCTGCTCAGACCTTGCGATGGCCAAATCAGCATC 609
Qy 201 IleGluHisGlnLysCysGluAsnAlaLysProGlyAsnIleThrAspThrMetValCys 220
Db 610 ATTGAGCACCAAGATGTGAGAACCCCTAACCCCGCAACATCACAGACCATGTGTGT 669
Qy 221 AlaSerValGlnGluGlyGlyLysAspSerCysGlnGlyAspSerGlyGlyProLeuVal 240
Db 670 GCCACCTGACAGAAAGGGGGCAAGGATCTCTGCGCAGGGTGACTCCGGGGGCCCTTGTG 729

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Qy 241 CysAsnGlnSerLeuGlnGlyIleLeuSerTrpGlyLysAspProCysAlaIleThrArg 260
Db 730 TGTAAACCGTCTCTTCAAGGATATATCTCCGGGGCAGAGATCCGTGCGATACCCGA 789
Qy 261 LysProGlyValTyrThrLysValCysLysTrpValAspTrpIleGlnGluThrMetLys 280
Db 790 AAGCTGTGTCTACAGAAAGTCTGCMAATATGTGACTGATTCAGAGACATGAG 849
Qy 281 AsnAsn 282
Db 850 AACAAAT 855

RESULT 6
US-10-140-021-505
; Sequence 505, Application US/10140021
; Publication No. US2003013886A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Geo, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Matanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C167
; CURRENT APPLICATION NUMBER: US/10/140,021
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-140-021-505

Alignment Scores:
Pred. No.: 5,19e-162 Length: 1204
Score: 1523.00 Matches: 282
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-856-320A-2 (1-282) x US-10-140-021-505 (1-1204)

Qy 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaAla 20
Db 10 ATGCAGAGGTTCAGGTGCTGGCGGAGCATGAGATCATCGGAGAGTCTCACAGCAGC 69
Qy 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgGlyLeuGlnLeu 40
Db 70 AAGGAACCTGGGGCCGCTCTCCCTCCAGGCGCATGAGATTCAGTTAATCTCG 129
Qy 41 LeuAlaLeuAlaThrGlyLeuValGlyGluThrArgGlyLeuLysGlyPheGluCys 60
Db 130 CTGCTCTGGCAGACGGGCTTGTAGGGGAGAGACAGGATATCAAGGGGTTCAAGTGC 189
Qy 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGluLysThrArgLeuLysGly 80
Db 190 AAGCTCACTCCAGCCCTGGGAGGAGCCCTGTTGAGAAAGACCGGCTACTGTGG 249

```

```

QY      81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuIysProArgTyr 100
      250 GCGAGCCTCATGCCCCCGATGGCTCTGACAGCAGCCACCTGCTCAAGCCCCCTAC 309
QY      101 IleValHisLeuGlyGlnHisAsnLeuGlnIlyGlyGlnGlnThrArgTyr 120
      310 ATAGTTCACCTGGGCGAGCACAACCTCCAGAAAGAGAGGGGTGTGAGCAGACCCGAC 369
QY      121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnIysAspHisArg 140
      370 GCCACTGAGCTCTTCCCCCACTCCGGCTTCAACAAAGAGCTCCCAACAAAGCAGCC 429
QY      141 AsnAspIleMetLeuValIysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
      430 AATGACATCATGTGTGTGAAGATGGCATGCCAGTCTTCATCATCCTGGGCTGTGCGACCC 489
QY      161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
      490 CTCACCCCTCTCCTCAGCTGTGTCACTGCTGGCAGCAGCTGCTATTTCCGGCTGGGG 549
QY      181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
      550 ACGACGTCAGCCCCCAAGTTAGCCCTGCTCACACCTTGAGTGCAGCCCAATCACCATC 609
QY      201 IleGlnHisGlnIlyCysGlnAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220
      610 ATTGACACCAAGAGTGTAGAGAGGCTTACCCCGGCAACATCAACACCATGGTGT 669
QY      221 AlaSerValGlnGlnIlyGlyIysAspSerCysGlnIlyAspSerGlyIlyProLeuVal 240
      670 GCCAGGCTCAGAAAGGGGCAAGAGACTCTGCGCAGGGTGAATCCGGGGGCTCTGGTGC 729
QY      241 CysAsnGlnSerLeuGlnIlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
      730 TGTAAACATCTCTTCAAGGCAATATCTCTGGGGCAGAGATCCGGTGCATGCCCA 789
QY      261 LysProGlyValTyrThrIysValCysIlyIysValAspTrpIleGlnGlnThrMetIys 280
      790 AAGCTGTGTCTACAGAAAGTCTGCATAATATGTGACTGATCCAGAGACGATGAAG 849
QY      281 AsnAsn 282
      850 AACAAAT 855
Db

```

RESULT 7
US-10-140-274-505
Sequence 505, Application US/10140274
Publication No. US20030143674A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Neureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C161
CURRENT APPLICATION NUMBER: US/10/140,274
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See File Wrapper or Palm

```

; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-274-505

Alignment Scores:
Pred. No.: 5,19e-162 Length: 1204
Score: 1523.00 Matches: 282
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-856-320A-2 (1-282) x US-10-140-274-505 (1-1204)
QY      1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaAla 20
      10 ATGCAAGAGTTAGAGTGGCTGGCGGACTGGAAAGTCATCGGCGAGAGGTCTTCACAGACCC 69
QY      21 LysGlnProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleLeu 40
      70 AAGCAACCTGGGGCCCGCTCTCCCTCCAGCCATGAGAGATTCTGCAGTTAATCTTG 129
QY      41 LeuAlaLeuAlaThrGlyLeuValGlyGlyGlyTrpArgIleIleIlyGlyIlyPheGlyCys 60
      130 CTTGCTCTGGCAACAGGCTGTGTAGGGGAGAGACAGAGATATCAAGGGTTTCAGTGC 189
QY      61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlyIlyThrArgLeuLeuCysGly 80
      190 AAGCTCTACTCCACAGCCCTGGCAGGAGCCCTGTTGAGAAACACCGGCTACTCTGTGG 249
QY      81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuIysProArgTyr 100
      250 GCGAGGCTCATGCCCCCAGATGGCTCTGACAGACGCCACTGCTCAAGCCCCGCTAC 309
QY      101 IleValHisLeuGlyGlnHisAsnLeuGlnIlyGlyGlnGlnThrArgTyr 120
      310 ATAGTTCACCTGGGCGAGCACAACCTCCAGAAAGAGAGGGGTGTGAGCAGACCCGAC 369
QY      121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnIysAspHisArg 140
      370 GCCACTGAGTCTCTTCCCCCAGCCGCTTCAACAAACAGCTCTCCCAACAAACACACCC 429
QY      141 AsnAspIleMetLeuValIysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
      430 AATGACATCATGTGTGTGAAGATGGCATGCGCAGTCTCCATCATCACTGGGCTGTGGAACC 489
QY      161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
      490 CTCACCCCTCTCTCAAGCTGTGTCACTGTGGCAGCACACTGCTCTATTTCCGGCTGGGG 549
QY      181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
      550 ACGACGTCAGGCCCCCAAGTTAGCTGCTCTACACCTTGCGATGGGCCAACATCCATC 609
QY      201 IleGlnHisGlnIlyCysGlnAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220
      610 ATTGACACCAAGAGTGTGAAGAGCGCTACCCCGGCAACATCAAGACACCATGTGTGT 669
QY      221 AlaSerValGlnGlnIlyGlyIysAspSerCysGlnIlyAspSerGlyIlyProLeuVal 240
      670 GCCAGGCTCAGAAAGGGGCAAGAGACTCTGCCAGGGTGAATCCGGGGGCTCTGTGTC 729
QY      241 CysAsnGlnSerLeuGlnIlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
      730 TGTAAACATCTCTTCAAGGCAATATCTCTGGGGCAGAGATCTGTGCGATCCACCCGA 789
QY      261 LysProGlyValTyrThrIysValCysIlyIysValAspTrpIleGlnGlnThrMetIys 280
      790 AAGCTGTGTCTACAGAAAGTCTGCATAATATGTGACTGATCCAGAGACGATGAAG 849

```

QY 281 AsnAsn 282
DB 850 AACAAAT 855

RESULT 8

US-10-140-471-505
; Sequence 505, Application US/10140471
; Publication No. US20030138887A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C163
; CURRENT APPLICATION NUMBER: US/10/140,471
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-471-505

Alignment Scores:

Pred. No.: 5,19e-162 Length: 1204
Score: 1523.00 Matches: 282
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-856-320A-2 (1,282) x US-10-140-471-505 (1-1204)

QY 1 MetGlnAglLeuAlyrTrrLeuAArgAspTrpLysSerSerGlyAArgGlyLeuThraAla 20
DB 10 ATGCAGAGGTTGAGGTGGCTGGCGGAGCTGGAAGTATCGGGAGAGGTCTCACAGCAGCC 69
QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleu 40
DB 70 AAGGAACCTGGGGCCGCTCTCCCTCCAGGSCATGAGGATTCGTGAGTTAATCTG 129
QY 41 LeuAlaLeuAlaThGlyLeuValAlGlyGlnTrpArgIleIleLeuGlyPheGluCys 60
DB 130 CTGCTCTGGCAACAGGCTTGTAGGGGAGAGACAGAGTATCATCAAGGGTTCAGTGC 189
QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGluLysTrpArgLeuLeuCysGly 80
DB 190 AAGCTCTCACTCCACAGCTGAGGAGGAGCCCTGTTGAGAGAGACCGGCTACTCTGTGG 249
QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThraAlaHisCysLeuLysProArgTrp 100
DB 250 GCGAGGCTCATGCCCCAGATGGCTCTCTGACAGAGAGCCCTGCTCAAGCCCGCTAC 309
QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlnGluGlyCysGlnGlnThraArgThr 120
DB 310 ATAGTTCACTCTGGGAGACAGAACTCCAGAAAGAGAGGAGGCTGTGAGAGAGACCCGGACA 369

QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
DB 370 GCCACTGAGTCTTCCCTCCACCCGCGCTTCAACAAACAGCTCCCAAAAGACATCCGCG 429
QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
DB 430 AATGACATCATGCTGTGTGAAGATGGCATCGCAGTCTCCATCAGCTGGGCTGTGGAGCC 489
QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
DB 490 CTCACCTCTCTCAAGCTGTGTGACTGCTGGACACAGCTCCATTTCCGGCTGGGGC 549
QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
DB 550 AGCAGCTCACCCCAAGTTAGCTGTGCTACACCTTGCGATGGCCAGATCCACATCCATC 609
QY 201 IleGluHisGlnLysCysGluAsnAlaTrpProGlyAsnIleThrAspThrMetValCys 220
DB 610 ATTGACACACAGAAAGTGTGAAGACCCCTACCCCGGCAACATCACAGACATGCTGTGT 669
QY 221 AlaSerValGlnGlnGlyGlyLysAspSerCysGlnGlnLysAspSerGlyProLeuVal 240
DB 670 GCCAGCTGACAGAAAGGGGCAAGAGACTCTGCCAGGAGTACTCCGGGGGCTCTGTGTC 729
QY 241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
DB 730 TGTAAACAGTCTCTTCAAGGAGATTATCTCTGGGGCCAGAGATCCGTGCGATACCCGA 789
QY 261 LysProGlyValTrpThrLysValCysLysTrpValAspTrpIleGlnGluThrMetLys 280
DB 790 AAGCTGTGTCTACAGCAAAAGTCTGCMAATATGTGACTGATCCAGAGACATGAG 849
QY 281 AsnAsn 282
DB 850 AACAAAT 855

RESULT 9

US-10-140-807-505
; Sequence 505, Application US/10140807
; Publication No. US20030134354A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C174
; CURRENT APPLICATION NUMBER: US/10/140,807
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-807-505

Alignment Scores:

Pred. No.: 5,19e-162 Length: 1204

Score: 1523.00 Matches: 282
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 12 Gaps: 0

US-09-856-320A-2 (1-282) x US-10-140-922-505 (1-1204)

```

QY 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSeriGlyLeuThrAlaAla 20
DB 10 ATGCAGAGGTTGAGTGCGCTGCGGAGCTGGAAGTCAATCGGAGAGCTTCACAGCAGCC 69
QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgLLeuGlnLeu 40
DB 70 AAGGAACCTGGGGCCGGCTCTCCCTCCAGGCATAGAGATTCTGCAGTTAACTCG 129
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyLeuThrArgLLeuLysGlyPheGlyCys 60
DB 130 CTGTGCTCTGGCAACAGGGCTTGTAGGGGAGAGACCAAGATCATCAAGGGGTTGAGTGC 189
QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlnLysThrArgLeuLysGly 80
DB 190 AAGCTCACTCCAGCCCTGCGAGGAGCCCTGTTGAGAGAGCGGCTACTCTGTGG 249
QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
DB 250 GCGAGGCTCATGGCCCGGAGATGGCTCTGACAGCAGCCCACTGCTCAAGCCCGCTAC 309
QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlyGlyCysGlnThrArgThr 120
DB 310 ATAGTTCACCTGGGCGAGCAACAACCTCCAGAAAGAGAGAGGGCTGTGAGCAGACCCGACA 369
QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
DB 370 GCCACTGAGTCTTCCCTCCAGCCCGGCTTCAACAAGAGCTCCCAACAAGACCAAGCCGC 429
QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerLLeuThrAlaValArgPro 160
DB 430 AATGACATCATGTGTGTGAAGATGGCATGGCCAGTCTCCATCAGCTGGGCTGTGCAACC 489
QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuLLeuSerGlyTyrGly 180
DB 490 CTCACCTCTCCCTCAGCGCTGTGTCACTGGGACAGCAGCTGCTCATTTCCGGCTGGGC 549
QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnLLeuThrIle 200
DB 550 AGCAGCTCCAGCCCGGAGTTAGCGCTGCTCACACCTTCGATGGCCCAACATCACCATC 609
QY 201 IleGlnHisGlnLysCysGlnAsnAlaTyrProGlyAsnLLeuThrAspThrMetValCys 220
DB 610 ATTGAGCACCAAGAGTGTGAAGACGCTTACCCCGGACATCATCAGACACCATGTGTGT 669
QY 221 AlaSerValGlnGlyGlyLysAspSerCysGlnLysAspSerGlyLysProLeuVal 240
DB 670 GCCAGGCTCAGAGAGGGGCAAGGAGACTCTGCGAGGAGTGAATCCGGGGCCCTCGTGC 729
QY 241 CysAsnGlnSerLeuGlnLysLLeuSerTrpGlyGlnAspProCysAlaLLeuThrArg 260
DB 730 TTTAACCAATCTCTTCAAGGACATTAATCTCTGCGGCGAGATCCGTTGCGATCAACCCGA 789
QY 261 LysProGlyValTyrThrLysValCysLysTyrValAspTrpLLeuGlnLLeuThrMetLys 280
DB 790 AAGCTGTGTGTACACGAAGTGTGCAATATGTGACTGGATCCAGAGAGCGATGAAG 849
QY 281 AsnAsn 282
DB 850 AACCAAT 855

```

RESULT 10

US-10-140-922-505
 ; Sequence 505, Application US/10140922
 ; Publication No. US2003013889A1
 ; GENERAL INFORMATION:

```

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C179
; CURRENT APPLICATION NUMBER: US/10/140,922
; PRIORITY FILING DATE: 2002-05-07
; PRIOR APPLICATION removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-922-505

Alignment Scores:
Pred. No.: 5,19e-162 Length: 1204
Score: 1523.00 Matches: 282
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-856-320A-2 (1-282) x US-10-140-922-505 (1-1204)
QY 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSeriGlyLeuThrAlaAla 20
DB 10 ATGCAGAGGTTGAGTGCGCTGCGGAGCTGGAAGTCAATCGGAGAGCTTCACAGCAGCC 69
QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgLLeuGlnLeu 40
DB 70 AAGGAACCTGGGGCCGGCTCTCCCTCCAGGCATAGAGATTCTGCAGTTAACTCG 129
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyLeuThrArgLLeuLysGlyPheGlyCys 60
DB 130 CTGTGCTCTGGCAACAGGGCTTGTAGGGGAGAGACCAAGATCATCAAGGGGTTGAGTGC 189
QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlnLysThrArgLeuLysGly 80
DB 190 AAGCTCACTCCAGCCCTGCGAGGAGCCCTGTTGAGAGAGACCGGCTACTCTGTGG 249
QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
DB 250 GCGAGGCTCATGGCCCGGAGATGGCTCTGACAGACGCCCACTGCTCAAGCCCGCTAC 309
QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlyGlyCysGlnThrArgThr 120
DB 310 ATAGTTCACCTGGGCGAGCAACAACCTCCAGAAAGAGAGGGCTGTGAGCAGACCCGACA 369
QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
DB 370 GCCACTGAGTCTTCCCTCCAGCCCGGCTTCAACAAGACCAAGCTCCCAACAAGACCAAGCCGC 429
QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerLLeuThrAlaValArgPro 160
DB 430 AATGACATCATGTGTGTGAAGATGGCATGGCCAGTCTCCATCAGCTGGGCTGTGCAACC 489
QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuLLeuSerGlyTyrGly 180

```

```

Db      490 CTCACCTCTCTCTCAGCGTGTCTGCTGACACAGCTGCTTATTCGGCTGGGCG 549
Qy      181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
Db      550 AGCAGCTCCAGGCCCCCAGTTAGCGCTGCTCAGCACCCTTGCGATGGCCACATCCACATC 609
Qy      201 ILeGluHisGlnLysCysGlnAsnAlaTyrProGlnAsnIleThrAspThrMetValCys 220
Db      610 ATTGAGCACACGAAGTGTAGAAACGCTCCGCCGCAACATCAGACACCATGTGTGT 669
Qy      221 AlaSerValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 240
Db      670 GCCACGCTGCAGAAAGGGGGCAAGAGCTCTCTCCAGGGTACTCCGGGGGCTCTGTGTC 729
Qy      241 CysAsnGlnSerLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 260
Db      730 TGTAAACGAGTCTCTTCAAGGCAATTATCTCTGGGGCCAGGATCCGTTGTCCGATCACCCGA 789
Qy      261 LysProGlnValTyrThrLysValCysLysTyrValAspTyrIleGlnIleThrMetLys 280
Db      790 AAGCTGTGTGTCTACACGAAGCTGTGCAAAATATGTGACTGTGATCCAGAGACGATGAAG 849
Qy      281 AsnAsn 282
Db      850 AACCAAT 855

```

RESULT 11

```

US-10-140-924-505
; Sequence 505, Application US/10140924
; Publication No. US2003013435A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C177
; CURRENT APPLICATION NUMBER: US/10/140,924
; PRIORITY FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-924-505

```

Alignment Scores:

```

Pred. No.: 5,19e-162 Length: 1204
Score: 1523.00 Matches: 282
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

```

US-09-856-320A-2 (1-282) x US-10-140-924-505 (1-1204)

Qy 1 MetGlnArgLeuArgTyrPleuArgAspTyrLysSerSerGlyArgGlyLeuThrAlaIle 20

```

Db      10 ATGAGAGGTTGAGGTGCTCGGAGCTGAAAGTCATGGGCAAGAGTCTACAGCACCC 69
Qy      21 LysGluProGlnValArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeu 40
Db      70 AAGGAACTGGGGCCCGCTCTCTCCCTCCAGGCCATGAGAGATTCTGCATTATCTTG 129
Qy      41 LeuAlaLeuAlaThrGlyLeuValGlyGluThrArgIleIleLeuGlyPheGluCys 60
Db      130 CTGTGCTGCACAACAGGCGCTGTAGGGGAGAGACACAGATCATCAAGGGGTTCCAGTGC 189
Qy      61 LysProHisSerGlnProTyrGlnAlaAlaLeuPheGlnLysTyrArgLeuLeuCysGly 80
Db      190 AAGCTCATCTCCAGCCCTGAGAGACAGCCCTGTTGGAAGAGCGGGCTACTGTGGG 249
Qy      81 AlaThrLeuAlaAlaProArgTyrPleuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
Db      250 GCGAGGCTCATCGCCCCAGATGGCTCTGACAGAGCCCACTGCTCAAGCCCGCTAC 309
Qy      101 ILeValHisLeuGlyGlnHisAsnLeuGlnLysGlnGlnGlnGlnGlnGlnGlnGlnGln 120
Db      310 ATAGTTCACTGGGGCAGACACACCTCCAGAGAGAGGGGCTGTGACACAGCCGGACA 369
Qy      121 AlaThrGlnSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
Db      370 GCCACTGATCTCTCCCGCCAGCTTCAACAACAGCCTCCCAACAAGACCCACCGC 429
Qy      141 AsnAspIleMetLeuValSerIleMetAlaSerProValSerIleThrTyrAlaValArgPro 160
Db      430 AATGACATCATGCTGTGTGAAGATGGATCGGCAGTCTTCATCAGCTGGGCTGTGGACCC 489
Qy      161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTyrGly 180
Db      490 CTCACCTCTCTCTCAGCTGTGTCACTGTGACAGCCAGCTCCATATTCGGGCTGGGGCG 549
Qy      181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
Db      550 AGCAGCTCACGCCCCCGAGTTAGCGCTGCTCAGCACCCTTGCGATGGCCACATCCACATC 609
Qy      201 ILeGluHisGlnLysCysGlnAsnAlaTyrProGlnAsnIleThrAspThrMetValCys 220
Db      610 ATTGAGCACACGAAGTGTGAGAACGCTTACCCCGGCAACATCAGACACCATGTGTGT 669
Qy      221 AlaSerValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 240
Db      670 GCCACGCTGCAGAAAGGGGGCAAGAGCTCTCTCCAGGGTACTCCGGGGGCTCTGTGTC 729
Qy      241 CysAsnGlnSerLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 260
Db      730 TGTAAACGAGTCTCTTCAAGGCAATTATCTCTGGGGCCAGGATCCGTTGTCCGATCACCCGA 789
Qy      261 LysProGlnValTyrThrLysValCysLysTyrValAspTyrIleGlnIleThrMetLys 280
Db      790 AAGCTGTGTGTCTACACGAAGCTGTGCAAAATATGTGACTGTGATCCAGAGACGATGAAG 849
Qy      281 AsnAsn 282
Db      850 AACCAAT 855

```

RESULT 12

```

US-10-140-926-505
; Sequence 505, Application US/10140926
; Publication No. US2003013435A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.

```

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/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Sherwood, Steven
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Watanabe, Colin K
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P330R1C187
/ CURRENT APPLICATION NUMBER: US/10/140,926
/ PRIOR APPLICATION REMOVED - See File Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 550
/ SEQ ID NO 505
/ LENGTH: 1204
/ TYPE: DNA
/ ORGANISM: Homo Sapien
/ US-10-140-926-505

Alignment Scores:
Pred. No.: 5,19e-162 Length: 1204
Score: 1523.00 Matches: 282
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-856-320a-2 (1-282) x US-10-140-926-505 (1-1204)

QY 1 MetGlnArgLeuAlaArgTrpLeuAlaArgSerGlyArgGlyLeuThrAlaAla 20
DB 10 ATGCAGAGGTGAAGTGGCTGGCGGACTGAGAGTCAATCGGCGAGAGCTTCACAGCAGCC 69
QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeu 40
DB 70 AAGGAACCTGGGGCCGCTCTCCCTCCAGCCATGAGATTCTGCAGTTAACTCG 129
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyLeuThrArgIleIleLysGlyPheGluCys 60
DB 130 CTTCCTCTGGCAACAGGGCTTTAGAGGGGAGAGACCGAGATCATCAAGGGGTTCCGAGTGC 189
QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGluLeuThrArgLeuLeuCysGly 80
DB 190 AAGCCTCACTCCAGCCTGGGAGGAGCCCTGTTGAAAGACGGGCTACTCTGTGG 249
QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
DB 250 GCGAGCCTCATGCGCCCGCAGATGGCTCTGACAGCAGCCCACTGCTCAAGCCCGCTAC 309
QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlyGlyCysGluGlnThrArgThr 120
DB 310 ATATGTTCACTGGGCGGAGCAACCTCCAGAAAGAGAGAGGGCTGTAGCAGACCCGAGACA 369
QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
DB 370 GCCACGTGAGTCTTCCCGCAGCCCGGCTTCAACAAAGCCTCCCAACAAACCAACCCG 429
QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
DB 430 AATGACATATGCTGTGTAAGATGGCATGGCCAGTTCATCACTGCGGCTGTGCAGCC 489
QY 161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
DB 490 CTCACCTCTCTCTCAAGCTGTCTCACTGTGCGACACAGCTGCTCTATTCGCGCTGGG 549
QY 181 SerThrSerSerProGlnLeuArgLeuProHisSerThrLeuArgCysAlaAsnIleThrIle 200
DB 550 AGCAGCTTCAGCCCGCAGTTAGCGCTGCTCAACCTTGCGATGGCGCAACATCACCATC 609
QY 201 IleGluHisGlnLysCysGluAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220

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DB 610 ATTGAGCACCAGAGTGTGAGAAAGCGCTACCCCGGCAATCATCAGACCATGTTGTGT 669
QY 221 AlaSerValGlnGlyGlyLysAspSerCysGlnGlyAspSerGlyLysProLeuVal 240
DB 670 GCCACGCTGCAGAAAGGGGCAAGAGCTCTCCAGGGGAGTCCGGGGCCCTCTGTGTC 729
QY 241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
DB 730 TGTAACTGCTCTCTCAAGCATTATCTCTGGGCGCAGAGATCCGTGTGCATCACCCGA 789
QY 261 LysProGlyValTyrThrLysValCysLysTyrValAspTrpIleGlnIleThrMetLys 280
DB 790 AAGCCTGTGTCTACACGAAAGTGTGCAATATGTGTGACTGTGATCAGAGAGATGAAG 849
QY 281 AsnAsn 282
DB 850 AACCAAT 855

RESULT 13
US-10-141-698-505
/ Sequence 505, Application US/10/141698
/ Publication No. US20030134357A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Beresini, Maureen
/ APPLICANT: DeForge, Laura
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Sherwood, Steven
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Watanabe, Colin K
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P330R1C206
/ CURRENT APPLICATION NUMBER: US/10/141,698
/ PRIOR APPLICATION REMOVED - See Palm or File Wrapper
/ NUMBER OF SEQ ID NOS: 550
/ SEQ ID NO 505
/ LENGTH: 1204
/ TYPE: DNA
/ ORGANISM: Homo Sapien
/ US-10-141-698-505

Alignment Scores:
Pred. No.: 5,19e-162 Length: 1204
Score: 1523.00 Matches: 282
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-856-320a-2 (1-282) x US-10-141-698-505 (1-1204)

QY 1 MetGlnArgLeuAlaArgTrpLeuAlaArgSerGlyArgGlyLeuThrAlaAla 20
DB 10 ATGCAGAGGTGAAGTGGCTGGCGGACTGAGAGTCAATCGGCGAGAGCTTCACAGCAGCC 69
QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeu 40
DB 70 AAGGAACCTGGGGCCGCTCTCCCTCCAGCCATGAGATTCTGCAGTTAACTCG 129
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyLeuThrArgIleIleLysGlyPheGluCys 60

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Db      130 CTTCGCTGCGCAAGAGGCTTTAGGGGAGAGACCAAGATCATCAGGCTTCAGATGC 189
QY      61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlnLysThrArgLeuLeuCysGly 80
Db      190 AAGCTCATCTCCAGCCCTGCGAGGAGCCCTGTTGAGAAAGACCGGCTACTCTGTGGG 249
QY      81 AlaThrLeuLeuAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
Db      250 GCGAGCGCTCATGCCCCCGATGGCTCTCGACAGAGCCGCTGCTCAAGCCCGCTAC 309
QY      101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlnGlyCysGlyGlnThrArgThr 120
Db      310 ATAGTTCACTGGGCGAGACACACTCCGAAAGAGAGAGGCTGTGAGAGACCCGGACA 369
QY      121 AlaThrGlnSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
Db      370 GCGACTGAGTCTCTCCCGCCAGCCCGCTTCAACAACAGCCTCCCAACAAGACACCGC 429
QY      141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
Db      430 AATGACATCATGCTGCTGAAAGATGGCATGCGCATCTCCATCATCCTGGGCTGTGGACCC 489
QY      161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
Db      490 CTCACCTCTCTCTCAAGCTGTGTCACTGCTGCGACCAAGCTGCTCATTTCCGGCTGGGG 549
QY      181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
Db      550 AGCAGCTGCAGCCCGCCAGTTACGCTGCTGACACCTTGCGATGCGCAACATCACCATC 609
QY      201 IleGluHisGlnLysCysGlnAsnAlaTyrProGlyAsnIleThrAspThrMetAlaCys 220
Db      610 ATTGAGCACCAAGAGTGAGAAAGCCCTTACCCCGCAACATATACAGACACCATGGTGTGT 669
QY      221 AlaSerValGlnGlnGlyGlyLysAspSerCysGlnGlyLysAspSerGlyGlyProLeuVal 240
Db      670 GCCACGCTGCAGAAAGGGGGGCAAGGACTCTCCAGGGTGAATCCGGGGGCTCTGTGATC 729
QY      241 CysAsnGlnSerLeuGlnGlnIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
Db      730 TGTAAACGAGTCTCTTCAAGGCAATTATCTCTGGGGCCAGAGTCCGTGCGCATCACCGA 789
QY      261 LysProGlyValTyrThrLysValCysLysTyrValAspTrpIleGlnGlnThrMetLys 280
Db      790 AAGCTGTGTCTTACACGAAGTGTGCAATATGTGACTGATCAGAGACGATGAAG 849
QY      281 AsnAsn 282
Db      850 AACAAAT 855

RESULT 14
US-10-141-702-505
; Sequence 505, Application US/10141702
; Publication No. US20030134358A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Defoige, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

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; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P330R1C208
; CURRENT APPLICATION NUMBER: US/10/141,702
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO: 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-141-702-505

Alignment Scores:
Pred. No.: 5,19e-162 Length: 1204
Score: 1523.00 Matches: 282
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-856-320A-2 (1-282) x US-10-141-702-505 (1-1204)
QY      1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAla 20
Db      10 ATGCAAGAGTTGAGTGGCTGCGGACTGGAAGTCATCGGCAAGGCTTCACAGCAGCC 69
QY      21 LysGlnProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeu 40
Db      70 AAGAACCTGGGGGCGCCCTCTCCCGCCCTCCAGGCGCATGAGATTCGCACTTAACTCG 129
QY      41 LeuAlaLeuAlaThrGlyLeuValGlyGlyGlnThrArgIleIleLysGlyPheGluCys 60
Db      130 CTTCCTGCGCAACAGGCTTGTAGGGGAGAGACAGAGATCATCAAGGGGTGTGAGTGC 189
QY      61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlnLysTrpArgLeuLeuCysGly 80
Db      190 AAGCTCATCTCCAGCCCTGCGAGGAGCCCTGTTCGAAAGACCGGCTACTCTGTGGG 249
QY      81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
Db      250 GCGAGCTGCATCGCCCGCCAGATGCTCTCTGACACAGCCCACTCCCAAGCCCGCTAC 309
QY      101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlnGlyCysGlyGlnThrArgThr 120
Db      310 ATAGTTCACTGCGGGGAGACACACTTCAGAGGAGAGGGCTGTGAGCAGACCCGGACA 369
QY      121 AlaThrGlnSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
Db      370 GCGACTGAGTCTCTCCCGCCAGCCCGCTTCAACAACAGCCTCCCAACAAGACACCGC 429
QY      141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
Db      430 AATGACATCATGCTGCTGAAAGATGGCATGCGCATCTCCATCATCCTGGGCTGTGGACCC 489
QY      161 LeuThrLeuSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
Db      490 CTCACCTCTCTCTCAAGCTGTGTCACTGCTGCGACCAAGCTGCTCATTTCCGGCTGGGG 549
QY      181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
Db      550 AGCAGCTGCAGAAAGGGGGGCAAGGACTCTGCGAGGATGACTCCGGGGGCTCTGTGATC 729
QY      201 IleGluHisGlnLysCysGlnAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220
Db      610 ATTGAGCACCAAGAGTGTGAAAGCGCTTACCGCCCGCAACATCAACAGACCATGTGTGT 669
QY      221 AlaSerValGlnGlnGlyGlyLysAspSerCysGlnGlyLysAspSerGlyGlyProLeuVal 240
Db      670 GCGAGCTGCAGAAAGGGGGGCAAGGACTCTGCGAGGATGACTCCGGGGGCTCTGTGATC 729
QY      241 CysAsnGlnSerLeuGlnGlnIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
Db      730 TGTAAACGATCTCTTCAAGGCAATTATCTCTGGGGGCGAGATCGGTGTGATCACCGCA 789

```



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QY      261 LysProGlyValTyrThrLysValCysLysTyrValAspTrpIleGlnGlnThrMetLys 280
DB      790 AAGCCGTGCTGTACTACAGAAAGCTCTCAATATATGTGACTGATCCAGAGAGATGAAG 849

QY      281 AsnAsn 282
DB      850 AACAAAT 855

RESULT 15
US-10-141-704-505
; Sequence 505, Application US/10141704
; Publication No. US20030134359A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Guiney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C209
; CURRENT APPLICATION NUMBER: US/10/141,704
; PRIOR PILING DATE: 2002-05-08
; PRIOR Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 505
; LENGTH: 1204
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-141-704-505

Alignment Scores:
Pred. No.:      5,19e-162      length:      1204
Score:          1523.00      Matches:      282
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             12          Gaps:           0

US-09-856-320A-2 (1-282) x US-10-141-704-505 (1-1204)
QY      1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyArgGlyLeuThrAlaAla 20
DB      10 ATGCAGAGGTTGAGTGAGGCTGCGGAGCTGGAAGTCATCGGCGAGAGCTTCACACAGACC 69
QY      21 LysGluProGlyAlaIahSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleLeu 40
DB      70 AAGGAACCTGGGGCCGCTCTCCCTCCCTCCAGGCGCATGAGATTCTGCAGTTAATCCCG 129
QY      41 LeuAlaLeuAlaThrGlyLeuValGlyGlyIuThrArgIleIleLysGlyPheGluCys 60
DB      130 CTTCCTCTGGCAACAGGGCTTTAGGGGAGAGACCAGGATCATCAAGGGGTTGAGGTGC 189
QY      61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGluLysThrArgLeuLeuCysGly 80
DB      190 AAGCTCACTCCAGGCTGCGCAGGAGGCTGTTGAGAAAGACCGGGCTACTCTGTGGG 249
QY      81 AlaThrLeuIleAlaIAProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
DB      250 GCGAGGCTCATGCCCCCGATGGCTCTGACAGACAGCCCACTGCTCAAGCCCCGCTAC 309

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QY      101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGluGluCysGluGlnThrArgThr 120
DB      310 ATAGTTACCTCTGGGAGACACAACCTCCAGAAAGAGAGAGGCTGTGAGACAGACCCGGAGA 369
QY      121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
DB      370 GCCACTGAGTCTCTCCCTCCAGCCCGCTTCAACAAAGCTCCCAACAAAGACCAACCCG 429
QY      141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
DB      430 AATGACATCATCTGTGTGAAGATGCAATCGCAGTCTCCATCATCCTGGGGCTGTGCGACCC 489
QY      161 LeuThrLysSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
DB      490 CTCACCTCTCTCCTACGCGTGTCTACTGTGSCACCAAGTGTCTCATTTCCGGCTGGGGC 549
QY      181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
DB      550 AGCAGGTCCAGGCCCCAGTTAGCCTGCTGCCTCACACCTTGCGATGCGCCAAATCACACATC 609
QY      201 IleGluHisGlnLysCysGluAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220
DB      610 ATTGACACACCAAGATGTGAGAACCCCTTACCCCGCAACATCACAGACACCATGTGTGT 669
QY      221 AlaSerValGlnGluGlyGlyLysAspSerCysGlnGlyAspSerGlyGlyProLeuVal 240
DB      670 GCCACGTCGACAGAAAGGGGCAAGAGATCTCTGCCAGGATGACTCCGGGGGCTCTGTGTC 729
QY      241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
DB      730 TGTAACTCAGTCTCTTCAAGGCATTTATCTCTGGGGCCAGAGATCCGTGTGCGATCACCCGA 789
QY      261 LysProGlyValTyrThrLysValCysLysTyrValAspTrpIleGlnGlnThrMetLys 280
DB      790 AAGCTGTGTCTTACACAGAAAGTGTGCAAAATATGTGACTGTGATCCAGAGACGATGAAG 849
QY      281 AsnAsn 282
DB      850 AACAAAT 855

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Search completed: October 23, 2003, 19:28:16
Job time : 322.593 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 22, 2003, 15:49:37 ; Search time 16.5558 Seconds
(without alignments)
1638.073 Million cell updates/sec

Title: US-09-856-320A-2

Perfect score: 1523

Sequence: 1 MGRRLMRDPMWSSGRLTA.....GYTVCKYVDWIOETMKN 282

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 segs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	698.5	45.9	260	156559	neuropilin - mouse
2	618.5	40.6	261	A31136	tissue kallikrein
3	617.5	40.5	265	KQRT	tissue kallikrein
4	612	40.2	248	S55066	trypsin (EC 3.4.21
5	611.5	40.2	259	B31136	tissue kallikrein
6	611.5	40.2	261	NGMSG	7S nerve growth fa
7	604.5	39.7	263	SI5686	tissue kallikrein
8	602.5	39.6	246	TRRT2	trypsin (EC 3.4.21
9	601.5	39.5	261	A34079	tissue kallikrein
10	600.5	39.4	246	TRRT1	trypsin (EC 3.4.21
11	596.5	39.2	261	A29586	tissue kallikrein
12	595.5	39.1	259	KORTN	tonin (EC 3.4.21 -
13	595	39.1	261	A29745	tissue kallikrein
14	594	39.0	238	S31779	trypsin (EC 3.4.21
15	591.5	38.8	262	S45303	tissue kallikrein
16	585.5	38.4	246	B25528	trypsin (EC 3.4.21
17	585	38.4	261	A25606	tissue kallikrein
18	580.5	38.1	261	KOMSI	tissue kallikrein
19	580	38.1	231	TRGTR	trypsin (EC 3.4.21
20	580	38.1	262	KQRT	tissue kallikrein
21	578.5	38.0	244	A44284	tissue kallikrein
22	578	38.0	232	KQPG	tissue kallikrein
23	576	37.8	247	TRDG	trypsin (EC 3.4.21
24	572.5	37.6	257	S31772	tissue kallikrein
25	572.5	37.6	261	S01971	tissue kallikrein
26	571.5	37.5	253	A51968	serine proteinase
27	569	37.4	229	TRBOTR	trypsin (EC 3.4.21
28	567	37.2	247	A27547	trypsin (EC 3.4.21
29	565	37.1	243	A35871	trypsin (EC 3.4.21

30	565	37.1	256	1	NGMSA	7S nerve growth fa
31	564.5	37.1	261	2	A41020	tissue kallikrein
32	564	37.0	259	2	A29746	tissue kallikrein
33	563	37.0	247	2	S13813	trypsin (EC 3.4.21
34	563	37.0	248	2	S55067	trypsin (EC 3.4.21
35	562.5	36.9	261	1	A32297	semogelase (EC 3
36	559.5	36.7	261	1	S35711	semogelase (EC 3
37	559	36.7	242	2	S48489	trypsin (EC 3.4.21
38	559	36.7	247	2	S05494	trypsin (EC 3.4.21
39	558.5	36.7	259	2	D23863	tissue kallikrein
40	558.5	36.7	261	1	TRMSMS	tissue kallikrein
41	558	36.6	261	2	A24378	tissue kallikrein
42	556	36.5	246	1	TRDGC	trypsin (EC 3.4.21
43	555.5	36.5	231	2	S31778	trypsin (EC 3.4.21
44	553	36.3	261	2	JB0236	tissue kallikrein
45	551.5	36.2	239	2	A27207	tissue kallikrein

ALIGNMENTS

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RESULT 1
156559
neuropilin - mouse
C:Species: Mus musculus (house mouse)
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000
C:Accession: 156559
R:Chen, Z.L.; Yoshida, S.; Kato, K.; Momota, Y.; Suzuki, J.; Tanaka, T.; Ito, J.; Nishi,
J. Neurosci. 15, 5088-5097, 1995
A:Title: Expression and activity-dependent changes of a novel limbic-serine protease ger
A:Reference number: 156559; MUID:95348817; PMID:7623137
A:Accession: 156559
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-260 <RES>
A:Cross-references: GB:D0785; NID:91648847; PIDN:BA06451.1; PID:g1020091
C:Superfamily: trypsin; trypsin homology
F:33-252/Domain: trypsin homology <TRY>

Query Match          45.9%; Score 698.5; DB 2; Length 260;
Best Local Similarity 52.0%; Pred. No. 3.9e-54;
Matches 129; Conservative 35; Mismatches 77; Indels 7; Gaps 3;

QY 1LLALATLVGGER-----ITKRECKRPHSQPQALPEKTRLLCGATLIPRVLTA 93
    |||||
DB 13 ILLLFMGAMAGLTPTAQSCKILEGRECIPIHSQPWQALFQGERLLCGVLVDRWVLTAA 72
    |||||
QY 94 HCLKPRYIVHGOHNLQKEEGCEOTRTATSPFHPGFNNSLPNKDRNDIMLVKMASPVS 153
    |||||
DB 73 HCKKQKIVRIGDHSLSRDPQDEIQVAQSIQHFCTYNSNP-EDHSHDILIRLQNSAN 131
    |||||
QY 154 ITWAVRPLTLSSRCVTAGTSCILSGMSGTSSPOLRPLTLRCANITIIHOKCENAYRPN 213
    |||||
DB 132 LGDKVKPQVLANLCPKVGOKCIISGCGVTSPQENFPTLNCABEVKISQNKCEAYGCK 191
    |||||
QY 214 ITDPMVCAVQEGDSCQSPSGPLVNCOSLOGIISGQPCATTRKPRGVTVCKXYVD 273
    |||||
DB 192 ITBGMVCAQ-SSNGADTQDSGGLVCDGMLQGITSGSDPCGKPRKRGVTVKICRYTT 250
    |||||
QY 274 WIOETMKN 281
    |||||
DB 251 WIKTMDN 258
    |||||

RESULT 2
A31136
tissue kallikrein (EC 3.4.21.35) 7 precursor, submandibular - rat
M:Alternate names: glandular prokallikrein 7, submandibular; proteinase A
C:Species: Rattus norvegicus (Norway rat)
C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 22-Jun-1999
C:Accession: A31136; S10698; S10699; D41429; B41429; S09315
R:Chen, Y.P.; Chao, J.; Chao, L.
Biochemistry 27, 7189-7196, 1988
```



```

OY      94 HCLKPRVYIHLQOHNLQKEGCEQOTATPESFHPENFNSL-----PKXDRNIMLV 146
Db      69 HCATNTYQVLMRLNNLYDEPPRQAHFLVQSFPHPENFODLLINHTROPEQDSNDMLL 128

OY      147 KMASEVSITMAVRPLTLSSRCVTAGTSCISIGSGTSSPOLRLPHTLRCAINTIIEHOK 206
Db      129 HLSQPADITDGVKVIDLPRIEPRKVGSTCLASGSGITPGLIELSDDLLQCNIDLLSNEK 188

OY      207 ENAYRGNTITDPMVCAVSQEGSKDSQCGDSGGPLVCNQSLGGITISWODPCALTRKRGVY 266
Db      189 VEAHKEEVLDMLCGEMQGGKDXDTCKSDGSPILCNGVILQGITSMGFNCPGEBKPKGIY 248

OY      267 KVCXVVDIMQIETMKKN 282
Db      249 KLIKETPMIKEVMKEN 264

```

RESULT 4
S55066
trypsin (EC 3.4.21.4) II precursor, pancreatic (clone 2-P29) - chicken
N/Alternate names: trypsinogen II
C/Species: Gallus gallus (chicken)
C/Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 22-Jun-1999
C/Accession: S55066; S72347
R/Wang, K.; Gan, L.; Lee, I.; Hood, L.
Biochem. J. 307, 471-479, 1995
A/Title: Isolation and characterization of the chicken trypsinogen gene family
A/Reference number: S55065; MUID:95251611; PMID:7733885
A/Accession: S55066
A/Molecule type: mRNA
A/Residues: 1-248 <MAN1>
A/Cross-references: EMBL,U15157; NID:g603906; PIDN:AAAT9914.1; PID:g603907
A/Experimental source: clone 2-P29
A/Accession: S72347
A/Molecule type: DNA
A/Residues: 1-248 <MAN2>
A/Cross-references: EMBL,U15157; NID:g603906; PIDN:AAAT9914.1; PID:g603907
A/Experimental source: clone 2-P29
C/Superfamily: trypsin; trypsin homology
C/Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F.1-16/Domain: signal sequence #status predicted <SIG>
F.17-25/Domain: activation peptide #status predicted <APT>
F.26-248/Product: trypsin II #status predicted <MPT>
F.26-241/Domain: trypsin homology <TRY>
F.65,109,202/Active site: His, Asp, Ser #status predicted

Query Match	40.2%	Score 612	DB 2:	Length 246:
Best Local Similarity	48.2%	Pred. No. 1,6e-46:		
Matches	121:	Conservative 38:	Mismatches 82:	Indels 10:
			Gaps	5
OY	33	MRILDLT-LALATGLVGG--ETRIIKGFEEKPHSQPMQALFEKTRLLCGATLIAPRM	88	
Db	1	MKFLFLILSLCGAANAFFPGGADDDKTVGGYGTCPREHVPQVSL-NSGWHFGGSLINSOM	59	
OY	89	LITAAHCKLPRIYVHLGQHNLLKEKECECDTRTATESFHPHGFNLSLPNDKHNDILVYM	148	
Db	60	VLSAAHCKRSKRGVALLGEYINIVQDESEVYKRSSTVIRPKYSSITLN---NDIMILKTL	115	
OY	149	ASPVSITVAWRPLVLSRCVTNAGTSCLISGWSSTSPQULRPLHTRCANITIIIEHKCEN	208	
Db	116	ASAAVEYSADIDPIALFPSSCAKAGTECLISGMGNLTLSNGVNYELLQCLNAPLISDOECE	175	
OY	209	AYPGNITPTWCAASVOEGGKSDCOGDSGGPLVCNOSLQGIISMGDPCAITRKPQYTRY	268	
Db	176	AYPGDITSNMLCVGLLEGKSDCOGDSGGPVCNGLGELIVSMGLG-CALKGYPGYTRY	234	
OY	269	CKYVDMIQETM	279	
Db	235	CNYVDMIQETI	245	

tissue kallikrein (EC 3.4.21.35) 3 precursor, submandibular - rat
M.Alternate names: glandular prokallikrein 3, submandibular
C.Species: Rattus norvegicus (Norway rat)
C.Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 22-Jun-1999
C.Accession: B31136
R.Chen, Y.P.; Chao, J.; Chao, L.
Biochemistry 27, 7189-7196, 1988
A.Title: Molecular cloning and characterization of two rat renal kallikrein genes.
A.Reference number: A31136; MUID:8908074; PMID:2849980
A.Accession: B31136
A.Molecule type: DNA
A.Residues: 1-259 <CHE>
A.Cross-references: GB:M19648; GB:J02837; NID:9205002; PIDN:AA51640.1; PID:9205004
A.Note: the authors translated the codon GTC for residue 230 as Cys
C.Superfamily: trypsin; trypsin homology
C.Keywords: hydrolase; serine proteinase
F.1-18/Domain: signal sequence #status predicted <SIG>
F.19-259/Product: tissue prokallikrein 3, submandibular #status predicted <MAT>
F.25-251/Domain: trypsin homology <TRY>
F.63, 118, 211/Active site: His, Asp, Ser #status predicted

Query Match 40.2%; Score 611.5; DB 2; Length 259;
Best Local Similarity 43.4%; Pred. No. 1,8e-46;
Matches 112; Conservative 45; Mismatches 88; Indels 13; Gaps 3;

```

QY 36 LQILHLATATGTVG---GETRIIKGFECCKPHSGQWQALFEKTRLLCATLIIAPWMLT 91
Db 3 LQILFLVLSVGRIDAPAPGQGRVVGVGXCKEKNKGQWQAVI--NNRYLGGGVILIDPSWVIT 60
QY 92 AAHCLKPRYIYHLGQHNQKEBEGCQQTATIESFPHPCN-----NSLPNKDRNDIM 144
Db 61 AAHCYSHNYHYLLGNNNLFEKDEPFAQYVNVNQSFPHPYNPFPFMKNHTLFPQGDHSNDIM 120
QY 145 LVKMASPVSIIMAVRPLTLSSRCVTAGRSCILISGSGSTSSPOLRLPHTLRCANITIIHQ 204
Db 121 LHLHSEPADITDGKVIDLPTBEPRKVGSTCLASGSSSTKPLEMERPDLDQCNINILNSE 180
QY 205 KCENAYPGNITDTMYCASVQEGGKSDSCGDSGSGPLVNCOSLOGIISWGDPCAIRKPCV 264
Db 181 KCIKIAHTOMVADVMLCAGELGEGKXDTGNGDSGGPLLCGVLOGITISWSSVPCGETRPAI 240
QY 265 YTKVCKYVDWITQETMKNN 282
Db 241 YTKLIKFTSWIKVEVKNEN 258

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RESULT 6

NGMSG

7S nerve growth factor gamma chain (EC 3.4.21.-) precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 18-Dec-1981 #sequence revision 17-May-1985 #text change 18-Jun-1999

C:Accession: A91005; A90949; A93510; A92341; A00942; A21093; A22705

R:Evans, B.A.; Richards, R.I.

EMBO J. 4, 133-138, 1985

A:Title: Genes for the alpha and gamma subunits of mouse nerve growth factor are config

A:Reference number: A91005; MUID:85257431; PMID:3848339

A:Accession: A91005

A:Molecule type: DNA

A:Residues: 1-261 <EVA>

R:Ullrich, A.; Gray, A.; Wood, W.I.; Hayflick, J.; Seeburg, P.H.

DNA 3, 387-392, 1984

A:Title: Isolation of a cDNA clone coding for the gamma-subunit of mouse nerve growth fa

A:Reference number: A90949; MUID:85076169; PMID:6548955

A:Accession: A90949

A:Molecule type: mRNA

A:Residues: 1-261 <UL3>

A:Cross-references: GB:X01389; NID:953373; PIDN:CAA25645.1; PID:953374

R:Howles, P.N.; Dickinson, D.P.; DiCaprio, L.L.; Woodworth-Gutai, M.; Gross, K.W.

Nucleic Acids Res. 12, 2791-2805, 1984

A:Title: Use of a cDNA recombinant for the gamma-subunit of mouse nerve growth factor to

A:Reference number: A93510; MUID:84169573; PMID:6200835

A:Accession: A93510

A:Molecule type: mRNA


```

      115 SPVKLNARVATVALPSSCAPAGTQCLISGWNLTSSGVNPDLLQCLDAPLPLPOADCEAS 174
      210 YPGNITDPMVCAVVOEGKDCSCGDSGPGVYVNOISLOGIISWGQDPCAIRKRGVYTKVC 269
      175 YPGKITDMMVCVGFLEGGKDCSCGDSGPGVYVNOISLOGIISWGQDPCAIRKRGVYTKVC 233
      270 KYVDWIQETMKNN 282
      234 NYVDWIQDTIAAN 246

RESULT 9
A34079
tissue kallikrein (EC 3.4.21.35) P1 precursor - rat
N:Alternate names: kallikrein-related proteinase K8
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 22-Jun-1999
C/Accession: A34079; S10700
R:Brady, J.M.; Wines, D.R.; MacDonald, R.J.
Biochemistry 28, 5203-5210, 1989
A>Title: Expression of two kallikrein gene family members in the rat prostate.
A:Reference number: A34079; MUID:89352606; PMID:2765531
A:Accession: A34079
A:Status: preliminary
A:Molecule type: DNA; mRNA
A:Residues: 1-261 <CRA>
A:Cross-references: GB:M27215; GB:M27216; GB:M27217; NID:g206638; PIDN:AAA42036.1; PID:g
A:Experimental source: prostate
R:Blomj r, A.; Gutman, N.; Brillard, M.; Gauchier, F.
FEBS Lett. 265, 137-140, 1990
A>Title: Substrate specificity of two kallikrein family gene products isolated from the
A:Reference number: S10698; MUID:90306305; PMID:2194829
A:Accession: S10700
A:Molecule type: protein
A:Residues: 25-43;112-138 <ELM>
A:Experimental source: submaxillary gland
A>Note: 125-Lys was also found
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine proteinase
F:25-253/Domain: trypsin homology <TRY>
F:25-111/Product: tissue kallikrein P1 light chain #status experimental <MAT1>
F:112-261/Product: tissue kallikrein P1 heavy chain #status experimental <MAT2>
F:65,120,213/Active site: His, Asp, Ser #status predicted

Query Match 39.5%; Score 601.5; DB 2; Length 261;
Best Local Similarity 43.0%; Pred. No. 1.4e-45;
Matches 111; Conservative 46; Mismatches 90; Indels 11; Gaps 2;

      36 LQILILALATG---LVGETRIIKGECKPHSQPQWQALFEKTRLLCGATILAPRWLT 91
      3 LILFILILGWNDAAPPCQSRIIGFNCCKNSQPVAVYHNEPQCQGVILHPSWLT 62
      92 AAHCLKRYIVLHGOHNLQKEGCEQRTATSEFPHPGFNNSTP-----PNKDRNDIM 144
      63 AAHCVSVNVQVWLGRRNLLEDEPFAGHRLVSGSFPHGRLDILKHKTRKPGNDVNDLM 122
      145 LKMASPVSVITAVRPLTSSRCVTAGTSCILISGWSSTSPQRLPHTLRCANITIIHQ 204
      123 LHLKTPADITDGVKVIDPTEPRKYSTCLTSGWGSIPPLKWEFPDDILQCVNIHLISNE 182
      205 KCENAVPGNITDPMVCAVVOEGKDCSCGDSGPGVYVNOISLOGIISWGQDPCAIRKRPV 264
      183 KIKIAYNDVITVMLCAGMDGKDCIKGDSGPGVILCDGVLOGITISWGSMPGEPNKPSEV 242
      265 YTRKCVYVDWIQETMKNN 282
      243 YTKLIKFTSMKKVMKEN 260

RESULT 10
TRPTI
trypsin (EC 3.4.21.4) I precursor - rat
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N:Alternate names: trypsinogen I
C:Species: Rattus norvegicus (Norway rat)
C>Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 24-Sep-1999
C/Accession: B22657; A00948
R:Craik, C.S.; Choo, Q.L.; Swift, G.H.; Quinto, C.; MacDonald, R.J.; Rutter, W.J.
J. Biol. Chem. 259, 14255-14264, 1984
A>Title: Structure of two related rat pancreatic trypsin genes.
A:Reference number: A22657; MUID:85054880; PMID:6094547
A:Accession: B22657
A:Molecule type: DNA
A:Residues: 1-246 <CRA>
A:Cross-references: GB:J00778; NID:g206507; PIDN:AAA98518.1; PID:g206508
A>Note: the authors translated the codon ATC for residue 6 as Leu and GAC for residue 1
R:MacDonald, R.J.; Stary, S.J.; Swift, G.H.
J. Biol. Chem. 257, 9724-9732, 1982
A>Title: Two similar but nonallelic rat pancreatic trypsin genes. Nucleotide sequences o
A:Reference number: A00948; MUID:82265624; PMID:6896710
A:Accession: A00948
A:Molecule type: mRNA
A:Residues: 1-246 <MAC>
A:Cross-references: GB:J00778; NID:g206507; PIDN:AAA98518.1; PID:g206508
C/genetics:
A:introns: 14/1; 67/2; 152/1; 197/3
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-23/Domain: activation peptide #status predicted <AP1>
F:24-246/Product: trypsin I #status predicted <ENZ>
F:24-239/Domain: trypsin homology <TRY>
F:30-160,48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted
F:63,107,200/Active site: His, Asp, Ser #status predicted
F:75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Query Match 39.4%; Score 600.5; DB 1; Length 246;
Best Local Similarity 46.6%; Pred. No. 1.6e-45;
Matches 118; Conservative 40; Mismatches 88; Indels 7; Gaps 4;

      30 LQAMRIILQILALATGVLGGETRIIKGECKPHSQPQWQALFEKTRLLCGATILAPRWLT 89
      1 MSALILALVGAAPVPL-EDDKIVGGTTCHEHVPYVSL-NSGYHFGSGLINDQVW 58
      90 LTAHCLKRYIVLHGOHNLQKEGCEQRTATSEFPHPGFNNSTP-----PNKDRNDIMLVKMA 149
      59 VSAHCYKSRIVRGENHNINVLBEGDEQFINAKIKHPNYSWLTN-----NDIMLIKIS 114
      150 SPVSITWAVRPLTSSRCVTAGTSCILISGWSSTSPQRLPHTLRCANITIIHQKCEA 209
      115 SPVKLNARVAPVAPALPSACAPACTQCLISGWNLTSSGVNPDLLQCLDAPVLSQADCEAA 174
      210 YPGNITDPMVCAVVOEGKDCSCGDSGPGVYVNOISLOGIISWGQDPCAIRKRGVYTKVC 269
      175 YPGKITDMMVCVGFLEGGKDCSCGDSGPGVYVNOISLOGIISWGQDPCAIRKRGVYTKVC 233
      270 KYVDWIQETMKNN 282
      234 NYVDWIQDTIAAN 246

RESULT 11
A29586
tissue kallikrein (EC 3.4.21.35) hck-1 precursor - human
N:Alternate names: glandular kallikrein
C:Species: Homo sapiens (man)
C>Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 22-Jun-1999
C/Accession: A29586
R:Schedlich, L.J.; Bennetts, B.H.; Morris, B.J.
DNA 6, 429-437, 1987
A>Title: Primary structure of a human glandular kallikrein gene.
A:Reference number: A29586; MUID:88054467; PMID:2824146
A:Accession: A29586
A:Molecule type: DNA
A:Residues: 1-261 <SCH>
A:Cross-references: GB:M8157; NID:g186640; PIDN:AAA74454.1; PID:g386842
```


R. Blaber, M. J. Isaacson, P. J. Bradshaw, R. A. Biochemistry 26, 6742-6749, 1987
 A:Title: A complete cDNA sequence for the major epidermal growth factor binding protein
 A:Reference number: A29745; MUID:88107593; PMID:3322386
 A:Accession: A29745
 A:Molecule type: mRNA
 A:Residues: 1-261 <BLA>
 A:Cross-references: GB:M17962; NID:9192997; PIDN:AAA37541.1; PID:9309212
 R. Isaacson, P. J. Silverman, R. E. Blaber, M. J. Server, A. C. Nichols, R. A. Shooter, E. M. Biochemistry 26, 2082-2085, 1987
 A:Title: Epidermal growth factor binding protein: identification of a different protein.
 A:Reference number: A27120; MUID:87299636; PMID:3304419
 A:Accession: A27120
 A:Molecule type: protein
 A:Residues: 25-54;112-124, 'X',126-130;165-184, 'X',186-187, 'X',189-192 <ISA>
 R. Evans, B. A. Drinkwater, C. C. Richards, R. I. J. Biol. Chem. 262, 8027-8034, 1987
 A:Title: Mouse glandular kallikrein genes: Structure and partial sequence analysis of th
 A:Reference number: 155260; MUID:87250386; PMID:3036794
 A:Accession: 170015
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 70-122 <RES>
 A:Cross-references: GB:M16608; NID:9198500; PIDN:AAA39351.1; PID:9198506
 C:Comment: This sequence is one of approximately twenty-five members of a gene family on
 C:Genetics:
 A:Gene: KAL
 C:Superfamily: trypsin, trypsin homology
 C:Keywords: hydrolase; serine proteinase; zymogen
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-24/Domain: propeptide #status predicted <PRO>
 F:25-261/Product: tissue kallikrein MGK-9, submandibular #status experimental <MAT>
 F:65-120,213/Active site: His, Asp, Ser #status predicted

Query Match 39.1%; Score 595; DB 2; Length 261;
 Best Local Similarity 42.1%; Pred. No. 5,3e-45;
 Matches 110; Conservative 53; Mismatches 86; Indels 12; Gaps 3;

QY 33 MIIILILALATGLVG---ETRIKFECKPHSQPQALFEKTRLLGATLIAPRW 88
 DB 1 MFLL-ILFLLSLGGIDAAPVHVSIVGFCCKESQPHVAVRYNEYICGVLIDNW 59
 QY 89 LITAAHCKPRYIVHGOHNLQKEGCEOTRTATESFPHPGNNLSI-----PKDHRN 141
 DB 60 VITAAHCHYENKVSILGKNNLIEBESQOHLVSSFLHPGYNRSILHNNHHPEDYSN 119
 QY 142 DIMLVKMASPVASITVAVRPLTISRCAVTAAGTSLISGWSSTSSPOLRLPHTLRCAITII 201
 DB 120 DMLRLRSKPADITDVVKRIALPTEPRKLGSTCLASGWSSTTPFRQNAKDLQCVNLKL 179
 QY 202 ENQKEMAVPGNITPTMVAASVOEGKDSQCGDGGPLVNCOSLOGIISWGDDPCAIRTK 261
 DB 180 PNEEDGKAHIEKVTDMLCAGETDGGDKDCKGDSGGPLICDVGLOGITSWGFPCGEPKK 239
 QY 262 PGVYTKVCYVDMIOETMKN 282
 DB 240 PGVYTKLIKFTSWIKDTMAKN 260

RESULT 14
 S31779
 trypsin (EC 3.4.21.4) III precursor - Atlantic salmon (fragment)
 C:Species: Salmo salar (Atlantic salmon)
 C:Date: 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
 C:Accession: S66657; S31779
 R. Male, R. J. Lorens, J. B. Smalas, A. O. Torrisen, K. R. Eur. J. Biochem. 232, 677-685, 1995
 A:Title: Molecular cloning and characterization of anionic and cationic variants of try
 A:Reference number: S66657; MUID:96035508; PMID:7556223
 A:Accession: S66657
 A:Molecule type: mRNA
 A:Residues: 1-238 <MAL>

A:Cross-references: EMBL:X70074; NID:964387; PIDN:CAA9679.1; PID:964388
 C:Superfamily: trypsin, trypsin homology
 C:Keywords: hydrolase; serine proteinase
 F:1-7/Domain: signal sequence (fragment) #status predicted <SIG>
 F:8-15/Domain: activation peptide #status predicted <APR>
 F:16-238/Product: trypsin III #status predicted <MAT>
 F:16-231/Domain: trypsin homology <TRY>
 F:22-152,40-56,124-225,131-198,163-177,188-212/Disulfide bonds: #status predicted
 F:55,99,192/Active site: His, Asp, Ser #status predicted

Query Match 39.0%; Score 594; DB 2; Length 238;
 Best Local Similarity 46.3%; Pred. No. 5,8e-45;
 Matches 112; Conservative 39; Mismatches 85; Indels 6; Gaps 4;

QY 41 LALALGVGGERIRIKFECKPHSQPQALFEKTRLLGATLIAPRWLTAAHCKPRY 100
 DB 3 VAFAPRIDDEDKIVGVECKRNSASYASL-QSGYHFCGGSLISSTWVSAHCKRSR 61
 QY 101 IVHLGOHNLQKEGCEOTRTATESFPHPGNNLSLNNKDRNDIMLVKMASPVASITVAVRP 160
 DB 62 QVRLENNHIVNVEGTEQFIDSVKVMHDSYNSR--NLD--NDIMLIKSKRPASLSYST 117
 QY 161 LTLSSRCVTAAGTSLISGWSSTSSPOLRLPHTLRCAITIIHQKCNAYPGNITDTWVC 220
 DB 118 VALPSSCASSGTRCLVSGWNLSSSNVPTLRCLDPIILSSSCNSAYPQOITSNMFC 177
 QY 221 ASVOEGKDSQCGDGGPLVNCOSLOGIISWGDDPCAIRKPGVYTKYCVDMIOETMK 280
 DB 178 AGFMGKGDSQCGDGGPLVNCOSLOGIISWGDDPCAIRKPGVYTKYCVDMIOETMK 236
 QY 281 NN 282
 DB 237 SN 238

RESULT 15
 S45303
 tissue kallikrein (EC 3.4.21.35) precursor - dog
 C:Species: Canis lupus familiaris (dog)
 C:Date: 20-Oct-1994 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
 C:Accession: S45303; S38487
 R. Gauthier, E. R. Dumas, C. Chappdelain, P. Tremblay, R. R. Dube, J. Y. Biochim. Biophys. Acta 1218, 102-104, 1994
 A:Title: Characterization of canine pancreas kallikrein cDNA.
 A:Reference number: S45303; MUID:94250683; PMID:8193155
 A:Accession: S45303
 A:Molecule type: mRNA
 A:Residues: 1-261 <GAU>
 A:Cross-references: EMBL:X75479; NID:9414018; PIDN:CAA53210.1; PID:9414019
 C:Superfamily: trypsin, trypsin homology
 C:Keywords: hydrolase; serine proteinase
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-261/Product: tissue kallikrein #status predicted <MAT>
 F:25-253/Domain: trypsin homology <TRY>
 F:65,120,213/Active site: His, Asp, Ser #status predicted

Query Match 38.8%; Score 591.5; DB 2; Length 261;
 Best Local Similarity 43.6%; Pred. No. 1.1e-44;
 Matches 112; Conservative 46; Mismatches 86; Indels 13; Gaps 2;

QY 39 ILLALATGLVG-----ETRIKFECKPHSQPQALFEKTRLLGATLIAPRWLTA 92
 DB 4 LVLCLASLAGTGAAPVQSRILIGMDTKNSQPMQALHYSKFGCGGLVHPEWVTA 63
 QY 93 AHCLKPRYIVHGOHNLQKEGCEOTRTATESFPHPGNNLSI-----LPNKDHRNDIML 145
 DB 64 AHCINDNQWLGVNYLFHEHDTAQPVQVRSFPHENSLKKNHTLPREDVSHDML 123
 QY 146 VKMASPVASITVAVRPLTISRCAVTAAGTSLISGWSSTSSPOLRLPHTLRCAITIIHQK 205
 DB 124 LRLAEPQITDAVAVLPLTQEPQVSGTCYASGWSIEPDKFIYPDDIQLQCVDELISNDI 183
 QY 206 CENAYPGNITDTWVCASVOEGKDSQCGDGGPLVNCOSLOGIISWGDDPCAIRKPGVY 265

Db	184	CANAHSQKVTBFLCAGHLEGGKDTCTVBDGGPLICDGVLOGITSMGHVPCGSPNNPAVY	243
Oy	266	TKVCKYVDNIOETMKN	282
Db	244	TKVISHLEWIKETMTAN	260

Search completed: October 22, 2003, 15:53:45
Job time : 17.5558 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2003, 15:48:12 ; Search time 9.9346 Seconds
(without alignments)
1335.036 Million cell updates/sec

Title: US-09-856-320A-2

Perfect score: 1523
Sequence: 1 MORLRLRDMKSSGRGLTAA.....GYTVKVCYKVDWIQETMKNN 282

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1355	89.0	250	1 KLB_HUMAN	Q9UBX7 homo sapien
2	756	49.6	250	1 KLB_HUMAN	Q9UBX9 homo sapien
3	701.5	46.1	260	1 NRPN_RAT	O88780 rattus norv
4	698.5	45.9	260	1 NRPN_MOUSE	O61955 mus musculu
5	692.5	45.5	256	1 KLB_HUMAN	O9B2R5 homo sapien
6	690	45.3	260	1 KLB_HUMAN	O60259 homo sapien
7	687.5	45.1	277	1 KLB_HUMAN	Q9UKR3 homo sapien
8	650.5	42.7	293	1 KLB_HUMAN	Q9Y337 homo sapien
9	632.5	41.5	251	1 KLB_HUMAN	Q9P0G3 homo sapien
10	618.5	40.6	248	1 KLB_HUMAN	Q9UBR0 homo sapien
11	618.5	40.6	261	1 KLB_HUMAN	P36373 rattus norv
12	617.5	40.5	261	1 KLB_HUMAN	P00758 rattus norv
13	612	40.2	248	1 TRX3_CHICK	Q90629 gallus gall
14	611.5	40.2	259	1 KLB_RAT	P36376 rattus norv
15	611.5	40.2	261	1 KLB_MOUSE	P00756 mus musculu
16	604.5	39.7	263	1 KLB_PRANA	P12824 primomys nat
17	602.5	39.6	246	1 TRX2_RAT	P00763 rattus norv
18	601.5	39.5	261	1 KLB_RAT	P36374 rattus norv
19	600.5	39.4	246	1 TRX1_RAT	P00762 rattus norv
20	596.5	39.2	261	1 KLB_HUMAN	P20151 homo sapien
21	595.5	39.1	259	1 KLB_RAT	P00759 rattus norv
22	595	39.1	261	1 KLB_MOUSE	P15949 mus musculu
23	594	39.0	238	1 TRX3_SALSA	P15933 salmo salar
24	594	39.0	244	1 KLB_HUMAN	Q92876 homo sapien
25	586	38.5	261	1 KLB_MOUSE	P15947 mus musculu
26	585.5	38.4	246	1 TRX2_MOUSE	P07146 mus musculu
27	580.5	38.1	261	1 KLB_MOUSE	P00755 mus musculu
28	580	38.1	231	1 TRYP_PIG	P00761 sus scrofa
29	580	38.1	262	1 KLB_HUMAN	P06870 homo sapien
30	578.5	38.0	244	1 KLB_RAT	P36375 rattus norv
31	578.5	38.0	246	1 KLB_PIG	P00752 sus scrofa
32	576	37.8	247	1 TRX2_CANFA	P06872 canis faml
33	572.5	37.6	243	1 TRX1_BOVIN	P00760 bos taurus

34	572.5	37.6	257	1 KLB_MOUSE	O07276 macaca fasc
35	572.5	37.6	261	1 KLB_MOUSE	P15946 mus musculu
36	571.5	37.5	253	1 KLB_HUMAN	P49862 homo sapien
37	569	37.4	244	1 TRX2_XENLA	P70059 xenopus lae
38	567	37.2	247	1 TRX3_RAT	P08426 rattus norv
39	567	37.2	258	1 KLB_PAPHA	Q28773 papio hamad
40	565	37.1	243	1 TRX1_XENLA	P19799 xenopus lae
41	565	37.1	256	1 KLB_MOUSE	P00757 mus musculu
42	564.5	37.1	261	1 KLB_MOUSE	P36368 mus musculu
43	564	37.0	248	1 TRX1_CHICK	Q90627 gallus gall
44	564	37.0	259	1 KLB_MOUSE	P15948 mus musculu
45	563	37.0	247	1 TRX2_BOVIN	Q29463 bos taurus

ALIGNMENTS

RESULT 1	ID	KLKB_HUMAN	STANDARD	PRT	250 AA.
AC	Q9UBX7	O75837	Q9NS65		
DT	16-OCT-2001	(Rel. 40, Created)			
DT	16-OCT-2001	(Rel. 40, Last sequence update)			
DT	15-SEP-2003	(Rel. 42, Last annotation update)			
DE	Kallikrein 11 precursor (EC 3.4.21.-) (Hippocastin) (Trypsin-like protease).				
GN	KLK11 OR PRSS20 OR TLSP.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RC	TISSUE=Hippocampus;				
RX	MEDLINE=98438738; PubMed=9765601;				
RA	Yoshida S., Taniguchi M., Suemoto T., Oka T., He X.P., Shiosaka S.;				
RT	"CDNA cloning and expression of a novel serine protease, TLSP.";				
RL	Biochim. Biophys. Acta 1399:225-228(1998).				
RN	[2]				
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).				
RC	TISSUE=Hippocampus, and prostate;				
RX	MEDLINE=20329229; PubMed=10872828;				
RA	Mitsui S., Yamada T., Okui A., Komitani K., Uemura H., Yamaguchi N.;				
RT	"A novel isoform of a kallikrein-like protease, TLSP/PRSS20, is expressed in the human brain and prostate.";				
RL	Biochem. Biophys. Res. Commun. 272:205-211(2000).				
RN	[3]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RC	MEDLINE=20130117; PubMed=10662548;				
RA	Yousef G.M., Scortlas A., Diamandis E.P.;				
RT	"Genomic organization, mapping, tissue expression, and hormonal regulation of trypsin-like serine protease (TLSP PRSS20), a new member of the human kallikrein gene family.";				
RL	Genomics 63:88-96(2000).				
RN	[4]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RX	MEDLINE=20510030; PubMed=11054574;				
RA	Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.;				
RT	"Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region.";				
RL	Gene 257:119-130(2000).				
RN	[5]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RC	Lamerdin J.E., McCreedy P.M., Skowronski E., Viswanathan V.;				
RA	Burthart-Schultz K., Gordon L., Dias J., Ramirez M., Stiliwagen S.;				
RA	Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Gaines J.;				
RA	Danapan L., Erlar A., Christensen M., Georgescu A., Avila J., Liu S.;				
RA	Andreia T., Traubheim M., Atlix C., Amico-Keller G., Coefield J.;				
RA	Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.;				
RA	Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.;				
RA	Olsen A.S., Carriano A.V.;				
RT	"Sequence analysis of chromosome 19q13.4.";				

RL Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.
 RN [6].
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Testis;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stacieleco M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Locoellano N.A., Peters G.J., Abramson R.D., Molligh S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schultz J., Myers R.W.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
 CC -1- FUNCTION: POSSIBLE MULTIFUNCTIONAL PROTEASE. EFFICIENTLY CLEAVES
 BZ-PHE-ARG-4-METHYLCOMARYL-7-AMIDE, A KALLIKREIN SUBSTRATE, AND
 WEALY CLEAVES OTHER SUBSTRATES FOR KALLIKREIN AND TRYPSIN.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Name=1;
 CC IsoId=Q9UBX7-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9UBX7-2; Sequence=VSP_005402;
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, SKIN AND PROSTATE. ISOFORM
 1 IS EXPRESSED PREFERENTIALLY IN BRAIN; ISOFORM 2 IN PROSTATE.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
 CC
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 DR EMBL; AB012917; BAA33404.1; ALT_INT.
 DR EMBL; AB013730; BAA88713.1; -
 DR EMBL; AB041036; BAA96797.1; -
 DR EMBL; AF164623; AAD47815.1; -
 DR EMBL; AF243527; AAG33364.1; -
 DR EMBL; AC011473; AAG32257.1; -
 DR EMBL; BC022068; AAH22068.1; -
 DR HSSP; P00753; IDPO.
 DR MEROPS; S01.257; -
 DR Genew; HGNC:6359; KLK11.
 DR MIM; 604434; -
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR001254; Ser protease_Try.
 DR Pfam; PF00089; trypsin; 1
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; TRYP_SPC; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase. Serine protease. Glycoprotein. Signal. Zymogen.
 KW Alternative splicing.
 FT SIGNAL 1 18
 FT PROPEP 19 21 POTENTIAL.
 FT CHAIN 22 250 ACTIVATION PEPTIDE (POTENTIAL).
 FT ACT_SITE 62 62 KALLIKREIN 11.
 FT ACT_SITE 110 110 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 110 110 CHARGE RELAY SYSTEM (BY SIMILARITY).

FT ACT_SITE 203 203 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 28 163 BY SIMILARITY.
 FT DISULFID 47 63 BY SIMILARITY.
 FT DISULFID 135 237 BY SIMILARITY.
 FT DISULFID 142 209 BY SIMILARITY.
 FT DISULFID 174 188 BY SIMILARITY.
 FT DISULFID 199 224 BY SIMILARITY.
 FT CARBOHYD 99 99 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 1 1 M -> MORLRRLRDKSSGRLTAKEGASPSPLQAM
 (in isoform 2)
 FT SQ SEQUENCE 250 AA; 27466 MW; 192D910BBCDC7A56 CRC64;
 Query Match 89.0%; Score 1355; DB 1; Length 250;
 Best Local Similarity 100.0%; Pred. No. 2,4e-116;
 Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 33 MRIQLILALATGLVGGETRIIKGFECCKPHSQWQALFEKTRLLCGATLIAPRWLLTA 92
 DB 1 MRIQLILALATGLVGGETRIIKGFECCKPHSQWQALFEKTRLLCGATLIAPRWLLTA 60
 QY 93 AHCLKPRITVHLGQHNLOKEGCECQOTRTATSPFHPGNNLSLPKDHRNDIMLYKMASPV 152
 DB 61 AHCLKPRITVHLGQHNLOKEGCECQOTRTATSPFHPGNNLSLPKDHRNDIMLYKMASPV 120
 QY 153 SITMAVRPLTSSRCVPTAGTSCGISGWSSTSSPOLRLPHTLRCAITIIIEHQKCNAYPG 212
 DB 121 SITMAVRPLTSSRCVPTAGTSCGISGWSSTSSPOLRLPHTLRCAITIIIEHQKCNAYPG 180
 QY 213 NITDTMVCASVOEGSKSCQGDSCGPLVCNCSLOGIISWGDDPCALITRKPGVYTKCKYV 272
 DB 181 NITDTMVCASVOEGSKSCQGDSCGPLVCNCSLOGIISWGDDPCALITRKPGVYTKCKYV 240
 QY 273 DWIOETMKNN 282
 DB 241 DWIOETMKNN 250
 RESULT 2
 KLK9 HUMAN STANDARD; PRT; 250 AA.
 ID KLK9 HUMAN
 AC Q9UKQ9;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Kallikrein 9 precursor (EC 3.4.21.-) (Kallikrein-like protein 3) (KLK-
 L3).
 GN GN
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RP MEDLINE=20118156; PubMed=10652563;
 RA Yousef G.M., Luo L.-Y., Diamandis E.P.;
 RT "Identification of novel human kallikrein-like genes on chromosome
 19q13.3-q13.4.";
 RL Anticancer Res. 19:2843-2852(1999).
 RN (2)
 RP SEQUENCE FROM N.A.
 RP MEDLINE=20247258; PubMed=10783266;
 RA Yousef G.M., Diamandis E.P.;
 RT "The expanded human kallikrein gene family: locus characterization and
 molecular cloning of a new member, KLK-L3.";
 RL Genomics 65:184-194(2000).
 RN (3)
 RP SEQUENCE FROM N.A.
 RP MEDLINE=20510030; PubMed=11054574;
 RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,

RA Moss P., Paepker B., Wang K.,
 RT "Sequencing and expression analysis of the serine protease gene
 cluster located in chromosome 19q13 region."
 RL Gene 257:119-130 (2000).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Lameudin J.E., McCready P.M., Skowronski E., Viswanathan V.,
 RA Burkhardt-Schulz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Gaines J.,
 RA Dangnan L., Ertler A., Christensen M., Georgescu A., Ayala J., Liu S.,
 RA Andreise T., Trankheim M., Attix C., Amico-Keller G., Coefield J.,
 RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
 RA Atellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
 RA Olsen A.S., Carrano A.V.,
 RT "Sequence analysis of chromosome 19q13.4";
 RL Submitted (Oct-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -1- TISSUE SPECIFICITY: SKIN, THYMUS, TRACHEA, CEREBELLUM AND SPINAL
 CC CORD.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
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 CC -----
 DR EMBL: AF135026; AAD26427.2; -;
 DR EMBL: AF243527; AAG33362.1; -;
 DR EMBL: AC011473; AAG33255.1; -;
 DR HSSP: P00763; IDPO.
 DR MEROPS: S01.307; -;
 DR Genew: HGNC:6370; KLK9.
 DR MIM: 605504; -;
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0006508; P:proteolysis and peptidolysis; NAS.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001254; Ser:protease_Try.
 DR Pfam: PF00089; trypsin; I.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR SMART: SM00020; TRYP_SPC; 1.
 DR PROSITE: PS00240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 DR Hydroxylase; Serine protease; Glycoprotein; Signal.
 DR KMW SIGNAL 1 15
 FT CHAIN 16 250
 FT ACT_SITE 63 63 KALLIKREIN 9.
 FT ACT_SITE 111 111 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 204 204 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 204 204 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 29 164 BY SIMILARITY.
 FT DISULFID 48 64 BY SIMILARITY.
 FT DISULFID 136 238 BY SIMILARITY.
 FT DISULFID 143 210 BY SIMILARITY.
 FT DISULFID 175 189 BY SIMILARITY.
 FT DISULFID 200 225 BY SIMILARITY.
 FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 250 AA; 27512 MW; F2785245B063E98B CRC64;
 Query Match 49 6%; Score 756; DB 1; Length 250;
 Best Local Similarity 57.0%; Pred. No. 9.7e-62;
 Matches 138; Conservative 37; Mismatches 67; Indels 0; Gaps 0;
 Oy 40 LIALATGLVGEETRIIKGECKPSPQALFEKTRLLCGATLLAPRLTAACLKPR 99
 Db 9 LLSLAGHMDTRALGAEECRPNQAGFLHLTRFCGATLLSDRLTLAAACRKRY 68
 Oy 100 YIVHLGQNLQKEEGEGQTRTATESPHDGFNNLSFNKCHRDIMLVKVASFVSITWAVR 159

Db 69 LWRRLGHEHLIMKWECPQLFRVTFPPHDPFNKOLSANDDNDIMLRPLRQARLSPAVO 128
 Oy 160 PLTSSRCYTACGSCISQMGSTSSPOLPLPHTLRACANTTIEHOKCEANYPENITDPMV 219
 Db 129 PLNTSQTQVSPGQCLISGMAVSPKALFPYTLQCANISILENKLCHMAYPGHISDML 188
 Oy 220 CASVQCGKDSGCGSGGPGVLVQNSLQGIISQGDCAITRRKGVYTKYKVDWIQETM 279
 Db 189 CAGLWGGGSGSCQDSGGLVNCGLTAGVSGAEGFCSRRPRAVTSYCHYIDMIQEIIM 248
 Oy 280 KN 281
 Db 249 EN 250
 RESULT 3
 NRPN RAT STANDARD; PRT; 260 AA.
 ID NRPN RAT
 AC 088780;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neutropsin precursor (EC 3.4.21.-) (NP) (Kallikrein 8) (Brain serine
 DE protease 1).
 GN KLK8 OR PRSS19 OR NRPN OR BSP1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 ON NCBI_TaxID=10116;
 RX SEQUENCE FROM N.A.
 RP STRAIN=Fischer; TISSUE=Brain;
 RX MEDLINE=98389725; PubMed=9722524;
 RA Davies B.J., Pickard B.S., Steel M., Morris R.G.M., Lache R.,
 RT "Serine proteases in rodent hippocampus."
 RL J. Biol. Chem. 273:23004-23011 (1998).
 CC -1- FUNCTION: SUGGESTED TO BE INVOLVED IN KINDLING EPILEPTOGENESIS AND
 CC HIPPOCAMPAL PLASTICITY. HAS A STRONG PROTEOLYTIC ACTIVITY AGAINST
 CC FIBRONECTIN (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- TISSUE SPECIFICITY: RESTRICTED TO HIPPOCAMPUS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
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 CC -----
 DR EMBL: AJ005641; CA06643.1; -;
 DR HSSP: O61955; INPM.
 DR MEROPS: S01.244; -;
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001254; Ser:protease_Try.
 DR Pfam: PF00089; trypsin; I.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR SMART: SM00020; TRYP_SPC; 1.
 DR PROSITE: PS00240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 DR Hydroxylase; Serine protease; Glycoprotein; Zymogen; Signal.
 DR KMW SIGNAL 1 32
 FT CHAIN 29 32
 FT PROPEP 29 32
 FT CHAIN 33 260
 FT ACT_SITE 73 73 NEUROPSIN.
 FT ACT_SITE 120 120 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 212 212 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 39 173 BY SIMILARITY.
 FT DISULFID 58 74 BY SIMILARITY.
 FT DISULFID 145 246 BY SIMILARITY.

Query Match
 Best Local Similarity 52.4%; Score 701.5; DB 1; Length 260;
 Matches 129; Conservative 35; Mismatches 75; Indels 7; Gaps 3;

39 ILLALATGLVGETR-----IIKFECKEHPQSOPMQLAFKTRLLCGATLIAPRLTLTA 93
 13 ILLFLMGMAGLTRAGSKIIIEGCECKHSPQWQALFQGRILVCGVLVDNRVLTIA 72
 94 HCLKPRYIVHIGQHLQKEEGCEQRTATSPHPGPFNNLSPNKQHRNDIMLVKASPV 153
 73 HCKKQKYSVRLGDHSIQKREDEPEQIQRVARSIQHPCFNSSNP-EDHSHDILRLQNSAN 131
 154 ITWAVRPLTLSSRCVTAGTSCILSGWGTSSPOLRLPHLRCANITIIHQECENAYRPN 213
 132 LQDKVKEPLANLCPKVGQKCTISGWTSPQENFPNTLCAEVKISQNCERAYPK 191
 214 IEDTWCAVSGGKXSCGSGGGLVNCQSLQGIISWGDDPCATIRKPGVYTKYCKYVD 273
 192 ITGHWVCAQ-SSNGADTCQSGGGLVNCVGLGITTGSDPCGKREKGVYTKICRTYN 250
 274 WIOETM 279
 251 WIKTMM 256

RESULT 4
 NRPN MOUSE
 ID NRPN MOUSE STANDARD; PRT; 260 AA.
 AC Q61955;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neutropin precursor (EC 3.4.21.-) (NP) (Kallikrein 8).
 GN KLK8 OR PRSS19 OR NRPN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCB; TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Hippocampus;
 RX MEDLINE=95348817; PubMed=7623137;
 RA Chen Z.-L., Yoshida S., Kato K., Momota Y., Suzuki J., Tanaka T.,
 Ito J., Nishino H., Aimoto S., Kiyama H., Shiosaka S.;
 "Expression and activity-dependent changes of a novel limbic-serine
 protease gene in the hippocampus.";
 RT J. Neurosci. 15:5088-5097(1995).
 RN (2)
 RP SEQUENCE FROM N.A.
 RA Yoshida S., Hirata A., Inoue N., Shiosaka S.;
 "Cloning and assignment of mouse neutropin gene, Prss19 to chromosome
 7B4.";
 RT Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.
 RN (3)
 RP SEQUENCE OF N-TERMINUS, AND CHARACTERIZATION.
 RC STRAIN=BALB/c; TISSUE=Brain;
 RX MEDLINE=9825202; PubMed=9556608;
 RA Shimizu C., Yoshida S., Shibata M., Kato K., Momota Y., Matsumoto K.,
 Shiosaka T., Midorikawa R., Kamachi T., Kawabe A., Shiosaka S.;
 "Characterization of recombinant and brain neutropin, a
 plasticity-related serine protease.";
 RT J. Biol. Chem. 273:11189-11196(1998).
 RN (4)
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 33-257.
 RC TISSUE=Hippocampus;
 RX MEDLINE=99134351; PubMed=9933620;
 RA Kishi T., Kato M., Shimizu T., Kato K., Matsumoto K., Yoshida S.,

Shiosaka S., Hakoshima T.;
 "Crystal structure of neutropin, a hippocampal protease involved in
 kindling epileptogenesis.";
 RT J. Biol. Chem. 274:4220-4224(1999).
 RL J. Biol. Chem. 274:4220-4224(1999).
 CC -1- FUNCTION: SUGGESTED TO BE INVOLVED IN KINDLING EPILEPTOGENESIS AND
 HIPPOCAMPAL PLASTICITY. HAS A STRONG PROTEOLYTIC ACTIVITY AGAINST
 FIBROECTIN.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
 CC -1- ENZYME REGULATION: STRONGLY INHIBITED BY DIISOPROPYL
 FLUOROPHOSPHATE, LEUPEPTIN AND (4-AMIDINOPHENYL)METHANESULFONYL 1-
 FLUORIDE.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN THE LIMBIC SYSTEM OF
 MOUSE BRAIN AND IS LOCALIZED AT HIGHEST CONCENTRATION IN PYRAMIDAL
 NEURONS OF THE HIPPOCAMPAL CA1-3 SUBFIELDS.
 CC -1- MASS SPECTROMETRY: MW=26613; METHOD=MALDI; RANGE=29-260.
 CC -1- MASS SPECTROMETRY: MW=26229; METHOD=MALDI; RANGE=33-260.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL; D30785; BAA06451.1; -;
 CC EMBL; AB032202; BAA92435.1; -;
 CC PIR; I56559; I56559
 CC PDB; INPM; 23-MAR-99.
 CC MEROPS; S01.244; -;
 CC MGD; MGI:892018; KLK8.
 CC InterPro; IPR001314; Chymotrypsin.
 CC InterPro; IPR001254; Ser protease_Try.
 CC Pfam; PF00089; trypsin; 1.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC SMART; SM00020; TRYPSIN; 1.
 CC PROSITE; PS50240; TRYPSIN_DOM; 1.
 CC PROSITE; PS00134; TRYPSIN_HIS; 1.
 CC DR PROSITE; PS00135; TRYPSIN_SER; 1.
 CC KW Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal;
 KW 3D-structure.
 FT SIGNAL 1 28
 FT PROPEP 29 32
 FT ACT_SITE 33 260
 FT ACT_SITE 73 73
 FT ACT_SITE 120 120
 FT ACT_SITE 212 212
 FT ACT_SITE 39 173
 FT DISULFID 58 74
 FT DISULFID 145 246
 FT DISULFID 152 218
 FT DISULFID 184 198
 FT DISULFID 208 233
 FT CARBOHYD 110 110
 FT STRAND 34 34
 FT STRAND 37 38
 FT STRAND 41 42
 FT TURN 41 42
 FT TURN 45 46
 FT STRAND 47 52
 FT TURN 53 54
 FT STRAND 55 64
 FT TURN 65 66
 FT STRAND 67 70
 FT STRAND 72 74
 FT HELIX 77 77
 FT STRAND 80 83
 FT STRAND 87 87
 FT TURN 88 89
 FT STRAND 96 98
 FT STRAND 100 105
 FT TURN 107 108
 FT TURN 114 115

N-LINKED (GLCNAC. .) (POTENTIAL).
 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CHARGE RELAY SYSTEM (BY SIMILARITY).

Query Match	Best Local Similarity	Score	DB 1:	Length	DB 2:
Matches 129; Conservative 40; Mismatches 74; Indels 15; Gaps 4	50.0%;	62.5	DB 1:	256;	DB 2:
Query	256 AA;	28087 MW;	B5B8FD6022786B5	CRC64;	
Db	4	118	178	238	264
Qy	155	119	205	179	265
Db	239	YTKVCHYLEWIRETKRN	256		
Qy	265	YTKVCKYVDWIQETMKN	282		
Db	239	YTKVCHYLEWIRETKRN	256		
Qy	155	TWAVRPLTLSSRCVYAGTSLISMGSTN	-----SP--QLRPHPLTKANITITIEHQ	204	
Db	119	NPOVRPAVLPTRCPPHAGCAVSGGLVSHNPGTAGSPRSQVSLPTDLHCANISII	SDT	178	
Qy	205	KCENAVPPNITDPTWVCASVOEGKSCGSGSPVLCNLSGIIISWGDDPCATIRKPGV	264		
Db	179	SCDSYSPRLNTNTWYACAGAEAGAESCEGSDSGPLVCGILOGIVSMGDVPCDNTTKRGV	238		
Qy	265	YTKVCKYVDWIQETMKN	282		
Db	239	YTKVCHYLEWIRETKRN	256		
Qy	155	TWAVRPLTLSSRCVYAGTSLISMGSTN	-----SP--QLRPHPLTKANITITIEHQ	204	
Db	119	NPOVRPAVLPTRCPPHAGCAVSGGLVSHNPGTAGSPRSQVSLPTDLHCANISII	SDT	178	
Qy	205	KCENAVPPNITDPTWVCASVOEGKSCGSGSPVLCNLSGIIISWGDDPCATIRKPGV	264		
Db	179	SCDSYSPRLNTNTWYACAGAEAGAESCEGSDSGPLVCGILOGIVSMGDVPCDNTTKRGV	238		
Qy	265	YTKVCKYVDWIQETMKN	282		
Db	239	YTKVCHYLEWIRETKRN	256		
Qy	155	TWAVRPLTLSSRCVYAGTSLISMGSTN	-----SP--QLRPHPLTKANITITIEHQ	204	
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Qy	265	YTKVCKYVDWIQETMKN	282		
Db	239	YTKVCHYLEWIRETKRN	256		
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Db	119	NPOVRPAVLPTRCPPHAGCAVSGGLVSHNPGTAGSPRSQVSLPTDLHCANISII	SDT	178	
Qy	205	KCENAVPPNITDPTWVCASVOEGKSCGSGSPVLCNLSGIIISWGDDPCATIRKPGV	264		
Db	179	SCDSYSPRLNTNTWYACAGAEAGAESCEGSDSGPLVCGILOGIVSMGDVPCDNTTKRGV	238		
Qy	265	YTKVCKYVDWIQETMKN	282		
Db	239	YTKVCHYLEWIRETKRN	256		
Qy	155	TWAVRPLTLSSRCVYAGTSLISMGSTN	-----SP--QLRPHPLTKANITITIEHQ	204	
Db	119	NPOVRPAVLPTRCPPHAGCAVSGGLVSHNPGTAGSPRSQVSLPTDLHCANISII	SDT	178	
Qy	205	KCENAVPPNITDPTWVCASVOEGKSCGSGSPVLCNLSGIIISWGDDPCATIRKPGV	264		
Db	179	SCDSYSPRLNTNTWYACAGAEAGAESCEGSDSGPLVCGILOGIVSMGDVPCDNTTKRGV	238		
Qy	265	YTKVCKYVDWIQETMKN	282		
Db	239	YTKVCHYLEWIRETKRN	256		
Qy	155	TWAVRPLTLSSRCVYAGTSLISMGSTN	-----SP--QLRPHPLTKANITITIEHQ	204	
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Qy	205	KCENAVPPNITDPTWVCASVOEGKSCGSGSPVLCNLSGIIISWGDDPCATIRKPGV	264		
Db	179	SCDSYSPRLNTNTWYACAGAEAGAESCEGSDSGPLVCGILOGIVSMGDVPCDNTTKRGV	238		
Qy	265	YTKVCKYVDWIQETMKN	282		
Db	239	YTKVCHYLEWIRETKRN	256		
Qy	155	TWAVRPLTLSSRCVYAGTSLISMGSTN	-----SP--QLRPHPLTKANITITIEHQ	204	
Db	119	NPOVRPAVLPTRCPPHAGCAVSGGLVSHNPGTAGSPRSQVSLPTDLHCANISII	SDT	178	
Qy	205	KCENAVPPNITDPTWVCASVOEGKSCGSGSPVLCNLSGIIISWGDDPCATIRKPGV	264		
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Qy	265	YTKVCKYVDWIQETMKN	282		
Db	239	YTKVCHYLEWIRETKRN	256		
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Qy	205	KCENAVPPNITDPTWVCASVOEGKSCGSGSPVLCNLSGIIISWGDDPCATIRKPGV	264		
Db	179	SCDSYSPRLNTNTWYACAGAEAGAESCEGSDSGPLVCGILOGIVSMGDVPCDNTTKRGV	238		
Qy	265	YTKVCKYVDWIQETMKN	282		
Db	239	YTKVCHYLEWIRETKRN	256		
Qy	155	TWAVRPLTLSSRCVYAGTSLISMGSTN	-----SP--QLRPHPLTKANITITIEHQ	204	


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FT ACT SITE 120 120 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT SITE 212 212 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 39 173 BY SIMILARITY.
FT DISULFID 58 74 BY SIMILARITY.
FT DISULFID 145 246 BY SIMILARITY.
FT DISULFID 152 218 BY SIMILARITY.
FT DISULFID 184 198 BY SIMILARITY.
FT DISULFID 208 233 BY SIMILARITY.
FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 23 23 A -> AACGSLDLITLTYANLPCVHLNPMQSPQSHCRG
WRSNLPDPPA (in isoform 2).
SQ SEQUENCE 260 AA; 28048 MW; EF439E5B8C3E660 CRC64;

Query Match 45.3%; Score 690; DB 1; Length 260;
Best Local Similarity 49.2%; Pred. No. 1.1e-55;
Matches 125; Conservative 45; Mismatches 80; Indels 4; Gaps 3;

QY 26 RSSPLQAMRLIQLIL-ALATGLVGEETRIIRIKGFECKPHSOPMOALFEKTRLLCGATL 83
DB 3 RPRPRAAKTMWFLLLGAMAGHSRAOEDKVLGHECHQPHSQWQALALVGGQLLGGVVL 62
QY 84 IAPRWLLTAHCLKPRYIYHLGOHNLQKEBGCQRTTATESFPHPGFNNSLPNKDHNDI 143
DB 63 VGGNWWLTAHCKKPKYTVRLGDHSLQNKDGPQEIPIVQSIHPPCYNSS-DVEDHNHDL 121
QY 144 MLYKMASPVISITAVRPLTLSSRCVATGSSCLISGMSGSSPOLRLPHLRCAANTITIEH 203
DB 122 MLLQLDQASLGSKVPRISLADCTPGQKCTVSGWGTVSPENPDLNCEVAKIPFO 181
QY 204 OKCENAYPGNITDTWVCASVOEGSGDCSGSGPVCNOSLOGIISWGODPCAIRRKKG 263
DB 182 KCCEDAYPGQITDGMWCAGSSKGA-DTCGDSGGLVCGALGITSMSGSDPGCRSDXFG 240
QY 264 VYTKVCYVDWIOE 277
DB 241 VYTNICRYLDWIKK 254

RESULT 7
KLLD HUMAN STANDARD; PRT; 277 AA.
AC 09UKR3; Q9Y433;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Kallikrein 13 precursor (EC 3.4.21.-) (Kallikrein-like protein 4)
GN (KLLK-14).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=20229789; PubMed=10766816;
RA Yousef G.M., Chang A., Diamandis E.P.;
RT "Identification and characterization of KLLK-14, a new kallikrein-like
RT gene that appears to be down-regulated in breast cancer tissues.";
RL J. Biol. Chem. 275:11891-11898(2000).

(2)
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCreedy P.M., Skowronski E., Vivanathan V.,
RA Burkhart-Schultz K., Gordon L., Dias J., Ramirez W., Stillvaen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Ganes J.,
RA Danganan L., Ertler A., Christensen M., Georgescu A., Avila J., Liu S.,
RA Andeise T., Tranheim M., Altix C., Amico-Keller G., Coefield J.,
RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
RA Olsen A.S., Carraro A.V.;
RT "Sequence analysis of chromosome 19q13.4.";
RL Submitted (Oct-2000) to the EMBL/GenBank/DBA databases.

```

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RP SEQUENCE OF 1-180 FROM N.A.
RC TISSUE-Uterus;
RA Ansoorge W., Winkler U., Mewes H.-W., Casenhuber J., Wiemann S.;
RL Submitted (May-1999) to the EMBL/GenBank/DBA databases.
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN PROSTATE, BREAST, TESTIS AND
CC SALIVARY GLAND.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
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CC -----
DR EMBL; AF135024; AAD26425.2; -
DR EMBL; AC011473; AAG23259.1; -
DR EMBL; AL050220; CAB43320.1; ALT_INIT.
DR HSSP; P00763; IDPO.
DR MEROPS; S01.306; -
DR Genew; HGNC:6361; KLLK13.
DR MIM; 605505; -
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0005576; P:proteolysis and peptidolysis; NAS.
DR InterPro; IPR001254; Ser.protease_fam.
DR Pfam; PF00089; trypsin; 1.
DR SMART; SM00020; TRYP_SP; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolyase, Serine protease, Glycoprotein, Signal.
FT SIGNAL 1 16
FT CHAIN 17 277
FT ACT SITE 76 76 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT SITE 124 124 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 218 218 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 42 178 BY SIMILARITY.
FT DISULFID 61 77 BY SIMILARITY.
FT DISULFID 157 224 BY SIMILARITY.
FT DISULFID 189 203 BY SIMILARITY.
FT DISULFID 214 239 BY SIMILARITY.
FT CARBOHYD 30 30 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 225 225 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 170 180 VNYPTLQCAN -> GMHPHRPPEAP (IN REF. 3).
SQ SEQUENCE 277 AA; 30570 MW; BA8A9E8DCFB5D542 CRC64;

Query Match 45.1%; Score 687.5; DB 1; Length 277;
Best Local Similarity 48.5%; Pred. No. 1.9e-55;
Matches 126; Conservative 48; Mismatches 71; Indels 15; Gaps 3;

QY 36 LQILALATGLVGG---ETRIK-----GFECKPHSOPMOALFEKTRLLCGA 81
DB 4 LALVALASLTLLALSGVSGSSKVLNTNGSTGFLPGGYTCFPHSQWQALALVGGLLCGG 63
QY 82 TLIAPRWLLTAHCLKPRYIYHLGOHNLQKEBGCQRTTATESFPHPGFNNSLPNKDHNDI 141
DB 64 VLVHKKWVLTAAHCKKPKYTVRLGDHSLQNKDGPQEIPIVQSIHPPCYNSS-DVEDHNHDL 123
QY 142 MLYKMASPVISITAVRPLTLSSRCVATGSSCLISGMSGSSPOLRLPHLRCAANTITIEH 200
DB 124 DIMLELDSPOVLGYIOTLPISHNNRLTPGTTCVSGWGTVSPENPDLNCEVAKIPFO 183
QY 201 IEHOKCENAYPGNITDTWVCASVOEGSGDCSGSGPVCNOSLOGIISWGODPCAIRRKKG 260
DB 184 RSDERCQVYVGKQITDNLKAGTKEGSGDCSGSGPVCNOSLOGIISWGODPCAIRRKKG 243
QY 261 KPGVYTKVCYVDWIOETMK 280
DB 244 RPYVTVRSYVLMIRETIR 263

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yousef G.M., Diamandis E.P.;
 RT "Molecular characterization, mapping, and tissue expression of KLK16,
 a hominoidally regulated kallikrein-like gene,"
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A. AND TISSUE SPECIFICITY.
 RX MEDLINE=21250997; PubMed=11352573;
 RA Hooper J.D., Butt L.T., Rae F.K., Harvey T.J., Myers S.A.,
 RA Ashworth L.K., Clements J.A.;
 RT "Identification and characterization of KLK14, a novel kallikrein
 serine protease gene located on human chromosome 19q13.4 and expressed
 in prostate and skeletal muscle,"
 RL Genomics 73:117-122(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Lamerdin J.E., McCreedy P.M., Skowronski E., Viswanathan V.,
 RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Ganes J.,
 RA Dangnan L., Eller A., Christensen M., Georgescu A., Avila J., Liu S.,
 RA Andeise T., Tranheim M., Altix C., Amico-Keller G., Coefield J.,
 RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
 RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
 RA Olsen A.S., Carraro A.V.;
 RT "Sequence analysis of chromosome 19q13.4,"
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP TISSUE SPECIFICITY.
 RX MEDLINE=20545474; PubMed=10969073;
 RA Harvey T.J., Hooper J.D., Myers S.A., Stephenson S.A., Ashworth L.K.,
 RA Clements J.A.;
 RT "Tissue-specific expression patterns and fine mapping of the human
 kallikrein (KLK) locus on proximal 19q13.4,"
 RL J. Biol. Chem. 275:37397-37406(2000).
 CC [1] SUBCELLULAR LOCATION: Secreted (Probable).
 CC [2] TISSUE SPECIFICITY: HIGH EXPRESSION IN BRAIN, BONE MARROW AND
 CC FETAL LIVER. ALSO EXPRESSED IN LIVER, PANCREAS, FETAL SPLEEN,
 CC PROSTATE AND SKELETAL MUSCLE.
 CC [3] SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
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 CC -----
 DR EMBL, AF161221, AAD50773.2, -;
 DR EMBL, AF283669, AAK48523.1, -;
 DR EMBL, AF283670, AAK48524.1, -;
 DR EMBL, AC011473, AAC23260.1, -;
 DR HSSP, P00763, IDPO.
 DR MEROPS, S01.029, -;
 DR Genew, HGNC:6362, KLK14.
 DR MIM, 606135, -;
 DR GO, GO:0005576, Cytoplasmic; NAS.
 DR GO, GO:0005508, Proteolysis and peptidolysis; NAS.
 DR InterPro, IPR001314, Chymotrypsin.
 DR InterPro, IPR001254, Ser. protease_Try.
 DR Pfam, PF00069, trypsin_1.
 DR PRINTS, PRO00722, CHYMOTRYPSIN.
 DR SMART, SM0020, Tryp_SPC_1.
 DR PROSITE, PS00240, TRYPSIN_DOM; 1.
 DR PROSITE, PS00134, TRYPSIN_HIS; 1.
 DR PROSITE, PS00135, TRYPSIN_SER; 1.
 KW Hydrolyase, Serine protease, Signal, Zymogen.
 FT SIGNAL 1 18
 FT PROPEP 19 24
 FT CHAIN 25 251
 KALLIKREIN 14.

FT ACT SITE 67 67 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 111 111 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 204 204 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 31 164 BY SIMILARITY.
 FT DISULFID 52 68 BY SIMILARITY.
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 FT DISULFID 175 189 BY SIMILARITY.
 FT DISULFID 200 225 BY SIMILARITY.
 SQ SEQUENCE 251 AA, 27452 MW, 9087953BAFA7ED25 CRC64;
 Query Match 41.5%; Score 632.5; DB 1; Length 251;
 Best Local Similarity 47.6%; Pred. No. 1,8e-50;
 Matches 118; Conservative 42; Mismatches 81; Indels 7; Gaps 3;
 QY 36 LQILALATGLVGETRIKPECKPHSQPQALF--EKTRLCGATLIPRLITTA 93
 DB 8 LQVLAIAM-TQSQEDENKIKGHTTTRSSQPQALALGPRRRFLCGGLALSGOWITAA 66
 QY 94 HCLKPRYIVHGOHNLQKEEGCEOTRTATSPFHPGFNNLSLPKNDIMLVKASPV 153
 DB 67 HGRPILOVALGKHLRREATQVLRVROVTHENVN---SRTHNDMLLQLOQPAR 122
 QY 154 ITMAVRPLTLSSRCVYTAGTSCILSGGSTSPQLRPLTLRCANITIIHQKCNAYPGN 213
 DB 123 IGRAVRPIEVTPQACASPGTSCVSGMTISSPIAYPASPLOCVNINISPDVCQKAYPT 182
 QY 214 ITDITWVCAVDEGGDCSCGDSGGLVYCNQSLGIIISNGDPCATRKRGVTKCKYVD 273
 DB 183 ITPGNVCAVDPGGKDCSGDSGGLVYCRQGLVSGMERCALPGYGVYTNLCYRS 242
 QY 274 WIOETMKN 281
 DB 243 WIEETMRD 250
 RESULT 10
 KKC HUMAN STANDARD; PRT; 248 AA.
 ID KKC HUMAN
 AC QYUKRQ, QYUKR1; Rel. 40, Created
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Kallikrein 12 precursor (EC 3.4.21.-) (Kallikrein-like protein 5)
 DE (KIK-15).
 GN KLK12 OR KLK15.
 OS Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=20118156; PubMed=10652563;
 RA Yousef G.M., Luo L.-Y., Diamandis E.P.;
 RT "Identification of novel human kallikrein-like genes on chromosome
 RT 19q13.3-q13.4,"
 RL Anticancer Res. 19:2843-2852(1999).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RA Yousef G.M., Magklara A., Scortilas A., Diamandis E.P.;
 RT "Cloning of new alternatively spliced forms of the kallikrein-like
 RT gene 5 (KIK-15),"
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=20510030; PubMed=11054574;
 RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCaig J.,
 RA Moss P., Paepel B., Wang K.;
 RT "Sequencing and expression analysis of the serine protease gene
 RT cluster located in chromosome 19q13 region,"
 RL Gene 257:119-130(2000).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RA Lamerdin J.E., McCreedy P.M., Skowronski E., Viswanathan V.,

RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Ganes J.,
 RA Dandapani L., Eiler A., Christensen M., Georgescu A., Avila J., Liu S.,
 RA Andreise T., Tranheim M., Attix C., Amico-Keller G., Coefield J.,
 RA Duare S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
 RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
 RA Olsen A.S., Carrano A.V.,
 RT "Sequence analysis of chromosome 19q13.4."
 RL Submitted (Oct-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q9UKR0-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9UKR0-2; Sequence=VSP_005403;
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL, AF135025; AAD26426.2; -;
 CC EMBL, AF135025; AAF06065.1; -;
 CC EMBL, AF243527; AAG33365.1; -;
 CC EMBL, AC011473; AAG23258.1; -;
 CC HSSP, P00763; IDPO.
 CC MEROPS, S01.020; -;
 CC GeneW, HGNC:6360; KLIK12.
 CC MIM, 605539; -;
 CC GO: GO:0005576; C:extracellular; NAS.
 CC GO: GO:0006508; P:proteolysis and peptidolysis; NAS.
 CC InterPro: IPR001254; Ser:protease_Try.
 CC Pfam: PF00089; trypsin; 1.
 CC SMART, SM00020; TRYP_SPC; 1.
 CC PROSITE, PS50240; TRYP_SIN_DOM; 1.
 CC PROSITE, PS00134; TRYP_SIN_HIS; 1.
 CC PROSITE, PS00135; TRYP_SIN_SER; 1.
 CC KW Hydrolase; Serine protease; Glycoprotein; Signal;
 CC Alternative splicing;
 CC FT SIGNAL 1 17
 CC FT CHAIN 18 248
 CC FT ACT_SITE 62 62 KALLIKREIN 12.
 CC FT ACT_SITE 108 108 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC FT ACT_SITE 200 200 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC FT DISULFID 28 161
 CC FT DISULFID 47 63 BY SIMILARITY.
 CC FT DISULFID 133 235 BY SIMILARITY.
 CC FT DISULFID 140 206 BY SIMILARITY.
 CC FT DISULFID 172 186 BY SIMILARITY.
 CC FT DISULFID 196 222 BY SIMILARITY.
 CC FT CARBOHYD 24 24 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT VARSPLIC 236 248 KYVDWIRIMRN -> NSTLVLGTSWNFNSQCP (1n
 CC isoform 2).
 CC /FTId=VSP_005403.
 CC SEQUENCE 248 AA; 26733 MW; BB473B98FBAF03 CRC64;
 CC Query Match 40.6%; Score 618.5; DB 1; Length 248;
 CC Best Local Similarity 48.2%; Pred. No. 3.3e-49;
 CC Matches 120; Conservative 35; Mismatches 89; Indels 5; Gaps 4;

QY 155 TWAVRPLTLSSRCVYTAGTSCILSGWSTSSQQLRPLPHTLRCAANTITIEHQECENAYPGNI 214
 DB 121 TSSVQPLPLPNDCAITAGTCHVSGMGLTNHPRNFPDLOCLNTSIVSHATCHGVYPPRI 180
 QY 215 TDTWVCASVQSGKSGCGSGPLVQNSIQGIISWGC-DPCALTRPGYTVKCKYVD 273
 DB 161 TSNMVCAG-GVPGQDAGCGSGPLVCGVQLQGLVSGSVGPPCGDGIIPGYTTIICKYVD 239
 QY 274 WIOETMKNN 282
 DB 240 WIRIMIRNN 248
 RESULT 11
 KIK7 RAT
 ID KIK7 RAT STANDARD; PRT; 261 AA.
 AC P36373;
 DT 01-UN-1994 (Rel. 29, Created)
 DT 01-UN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Glutathione S-transferase 7, submandibular/renal precursor (EC 3.4.21.35)
 DE (Tissue kallikrein) (RKG-7) (RSG-7) (Esterase B) (Proteinase A).
 GN KIK7 OR KIK-7
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8908074; PubMed=2849988;
 RA Chen Y.-P., Chao J., Chao L.;
 RT "Molecular cloning and characterization of two rat renal kallikrein
 RT genes."
 RT J. Biochemistry 27:7189-7196(1988).
 RL Biochemistry 27:7189-7196(1988).
 RN [2]
 RP SEQUENCE OF 25-75.
 RC TISSUE=Submaxillary gland;
 RX MEDLINE=88198057; PubMed=3482210;
 RA Kato H., Nakamishi E., Enyoji K., Hayaishi I., Oh-Ishi S., Iwanaga S.;
 RT "Characterization of serine proteinases isolated from rat
 RT submaxillary gland: with special reference to the degradation of rat
 RT kininogens by these enzymes."
 RT J. Biochem. 102:1389-1404(1987).
 RL J. Biochem. 102:1389-1404(1987).
 CC -1- FUNCTION: GLANDULAR KALLIKREINS CLEAVE MET-LYS AND ARG-SER BONDS
 CC IN KININOGEN TO RELEASE LYS-BRADYKININ.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage of Arg-|-Xaa bonds in
 CC small molecule substrates. Highly selective action to release
 CC kallidin (lysyl-bradykinin) from kininogen involves hydrolysis of
 CC Met-|-Xaa or Leu-|-Xaa.
 CC -1- TISSUE SPECIFICITY: KIDNEY AND SUBMANDIBULAR GLAND.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL, M19647; AAA41461.1; -;
 CC PIR, A31136; A31136.
 CC HSSP, P00759; ITON.
 CC MEROPS, S01.406; -;
 CC InterPro: IPR001254; Ser:protease_Try.
 CC Pfam, PF00089; trypsin; 1.
 CC SMART, SM00020; TRYP_SPC; 1.
 CC PROSITE, PS50240; TRYP_SIN_DOM; 1.
 CC PROSITE, PS00134; TRYP_SIN_HIS; 1.
 CC PROSITE, PS00135; TRYP_SIN_SER; 1.
 CC KW Hydrolase; Serine protease; Glycoprotein; Multigene family; Zymogen;
 CC Signal.

Query Match	Best Local Similarity	40.5%	Score 617.5	DB 1	Length 261
RC	TISSUE=Kidney;				
RX	MEDLINE=89327211; PubMed=2753879;				
RA	Inoue H., Fukui K., Miyake Y.;				
RT	"Identification and structure of the rat true tissue kallikrein gene expressed in the kidney.";				
RL	J. Biochem. 105:834-840(1989).				
RP	[4]				
RN	SEQUENCE FROM N.A.				
RX	MEDLINE=89214217; PubMed=2708383;				
RA	Wines D.R., Brady J.M., Pitchett D.B., Roberts J.L., Macdonald R.J.;				
RT	"Organization and expression of the rat kallikrein gene family.";				
RL	J. Biol. Chem. 264:7653-7662(1989).				
RP	[5]				
RN	SEQUENCE OF 48-261 FROM N.A.				
RX	MEDLINE=86131678; PubMed=3004582;				
RA	Gerald W.L., Chao J., Chao L.;				
RT	"Immunological identification of rat tissue kallikrein cDNA and characterization of the kallikrein gene family.";				
RL	Biochim. Biophys. Acta 866:1-14(1986).				
CC	-1- FUNCTION: GLANDULAR KALLIKREINS CLEAVE MET-LYS AND ARG-SER BONDS				
CC	IN KININOGEN TO RELEASE LYS-BRAADYKININ.				
CC	-1- CATALYTIC ACTIVITY: Preferential cleavage of Arg- -Xaa bonds in				
CC	small molecule substrates. Highly selective action to release				
CC	kallidin (Lysyl-bradykinin) from kininogen involves hydrolysis of				
CC	Met- -Xaa or Leu- -Xaa.				
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.				
CC	-----				
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CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; J00758; -; NOT ANNOTATED CDS.				
DR	EMBL; M11563; AAA41464.1; ALT_INIT.				
DR	EMBL; M23876; AAA41462.1; -.				
DR	EMBL; M23874; AAA41462.1; JOINED.				
DR	EMBL; M23875; AAA41462.1; JOINED.				
DR	EMBL; D00448; BAA00346.1; JOINED.				
DR	EMBL; D00446; BAA00346.1; JOINED.				
DR	EMBL; D00447; BAA00346.1; JOINED.				
DR	EMBL; X03560; CAA27247.1; -.				
DR	PIR; A00944; KORTP.				
DR	HSSP; P00757; 1SGF.				
DR	MEROPS; S01.405; -.				
DR	InterPro; IPR001254; Ser_protease_Try.				
DR	Pfam; PF00089; trypsin.1.				
DR	SMART; SM00020; TRYP_SPC; 1.				
DR	PROSITE; PSS00240; TRYP_SIN_DOM; 1.				
DR	PROSITE; PS00134; TRYP_SIN_HIS; 1.				
DR	PROSITE; PS00135; TRYP_SIN_SER; 1.				
DR	Hydrolase; Serine protease; Glycoprotein; Multigene family; Zymogen;				
KW	Signal.				
FT	SIGNAL	1	18	PROBABLE.	
FT	PROPEP	19	24	ACTIVATION PEPTIDE (PROBABLE).	
FT	CHAIN	25	261	GLANDULAR KALLIKREIN 1.	
FT	CHAIN	25	111	CHAIN 1.	
FT	CHAIN	112	261	CHAIN 2.	
FT	ACT_SITE	65	65	CHARGE RELAY SYSTEM.	
FT	ACT_SITE	120	120	CHARGE RELAY SYSTEM.	
FT	ACT_SITE	213	213	CHARGE RELAY SYSTEM.	
FT	DISULFID	31	173	BY SIMILARITY.	
FT	DISULFID	50	66	BY SIMILARITY.	
FT	DISULFID	152	219	BY SIMILARITY.	
FT	DISULFID	184	198	BY SIMILARITY.	
FT	DISULFID	209	234	BY SIMILARITY.	
FT	CARBOHYD	108	108	N-LINKED (GLCNAC...) (PROBABLE).	
SO	SEQUENCE	261 AA;	28852 MW;	F2P9C0227A7882B CRC64;	

RESULT 13			
ID	TRY3_CHICK	STANDARD;	PRT; 248 AA.
AC	Q90629;		
DT	01-NOV-1997 (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	Trypsin II-P29 precursor (EC 3.4.21.4).		
OS	Gallus gallus (Chicken).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Archosauromia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;		
OC	Gallus.		
OX	NCBI_TaxID=9031;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Pancreas;		
RX	MEDLINE=95251611; PubMed=7733865;		
RA	Wang K., Gan L., Lee I., Hood L.E.;		
RT	"Isolation and characterization of the chicken trypsinogen gene family.";		
RL	Biochem. J. 307:471-479(1995).		
CC	-; CATALYTIC ACTIVITY: Preferential cleavage: Arg- -Xaa, Lys- -Xaa.		
CC	-; SUBCELLULAR LOCATION: Extracellular.		
CC	-; TISSUE SPECIFICITY: HIGH LEVELS ARE SEEN IN THE PANCREAS WHILE		
CC	LOWER LEVELS ARE FOUND IN THE LIVER, SPLEEN AND THYMUS.		
CC	-; SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.		
CC	-----		
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CC	-----		
DR	EMBL; U15157; AAA79914.1; -.		
DR	PIR; S5066; S55066.		
DR	HSSP; P00763; IDPO.		
DR	MEROPS; S01.151; -.		
DR	InterPro; IPR001254; Ser.protease_Try.		
DR	Pfam; PF00089; trypsin; 1.		
DR	SMART; SM00020; Tryp_Sec; 1.		
DR	PROSITE; PS0240; TRYPSIN_DOM; 1.		
DR	PROSITE; PS00134; TRYPSIN_SER; 1.		
DR	PROSITE; PS00135; TRYPSIN_SER; 1.		
KW	Hydrolase; Serine protease; Digestion; Pancreas; Zymogen; Signal;		
KW	MultiGene family.		
FT	SIGNAL	1	16
FT	PROPEP	17	25
FT	CHAIN	26	248
			BY SIMILARITY.
			ACTIVATION PEPTIDE (BY SIMILARITY).
			TRYPSIN II-P29.

QY 33 MRLOILT--LALALGVGG--ETRIILKGFCKHSDPQWQALAEKIRLLCGAIIAPRW 88
Db 1 MKFLFLILSCLGAAVAAPFGADDDDKIVGGYCPHSPAPYQVSL-NSGYHFCGGSLLINSOW 59
QY 89 LITAAHCLKPRIVYVLGQNIQKEGCGQQTATIESPPHFGPNNSLPNKHRNDIMLVK 148
Db 60 VISAACVYSRIRQVFLGEGYNIIDVQEDSEVWSSVIIIRHFPYSITLN---NDIMILIK 115
QY 149 ASPVSIITWAVREPLTISRCTAGTISCLISGWSSTSPQLRLPHLRCAITIIIEHKCN 208
Db 116 ASAVEISADIQIALPSSCAKAGTIECLISGMGNLTNSGNYVPELLOCLNAPLISDQCE 175
QY 209 AYPGNITDTMVCASVQEGGKDSCCQDSCGPLVNCSLQGIISWGQDPCAITRKPGYVTKY 268
Db 176 AYPGDITSMICVGLFEGGKDSCCQDSCGPLVNCSELQGIIVSWGIG-CALKGYPGVYTKY 214
QY 269 CKYVDIMQIETM 279
Db 235 CNIVDIQIETI 245

	RESULT 14		
CC	KLKRC_RAT		
ID	_KLKRC_RAT	STANDARD:	PRT; 259 AA.
AC	P36376;		
DT	01-JUN-1994 (Rel. 29, Created)		
DT	01-JUN-1994 (Rel. 29, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Glandular kallikrein 12, submandibular/renal precursor (EC 3.4.21.35)		
DE	(Tissue kallikrein) (RSCG-3).		
GN	KLK12 OR KLK-12.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.		
OX	NCB1_TaxId=10116;		
PN	[1] _SEQUENCE FROM N.A.		
RX	MEDLINE=89088074; PubMed=2849988;		
RA	Chen Y.-P., Chao J., Chao L.;		
RT	"Molecular cloning and characterization of two rat renal kallikrein		
RL	genes.";		
RT	Biochemistry 27:7189-7196(1988).		
CC	- FUNCTION: GLANDULAR KALLIKEIN CLEAVE MET-LYS AND ARG-SER BONDS		
CC	IN KININOGEN TO RELEASE LYS-BRADYKININ.		
CC	- CATALYTIC ACTIVITY: Preferential cleavage of Arg-Xaa bonds in		
CC	small molecule substrates. Highly selective action to release		
CC	kallidin (lysyl-bradykinin) from kininogen involves hydrolysis of		
CC	Met-Xaa or Leu-Xaa.		
CC	- TISSUE SPECIFICITY: KIDNEY AND SUBMANDIBULAR GLAND.		
CC	- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.		
CC	-----		
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CC -----
CC EMBL: M39648: AAA51640.1;
CC EMBL: M22922: AAA51640.1; JOINED.
CC PIR: B31136; B31136.
CC HSSP: P00759; ITON.
CC MEROPS: S01.160; -.
CC InterPro: IPR001254; Ser protease_Try.
CC Pfam: PF00089; trypsin.1.
CC SMART: SM00020; Tryp_Spc.1.
CC PROSITE: PS50240; TRYPSIN_DOM.1.
CC PROSITE: PS00134; TRYPSIN_HIS.1.
CC PROSITE: PS00135; TRYPSIN_SER.1.
CC K01 Hydroxylase; Serine protease; Glycoprotein; Multigene family; Zymogen;
CC Signal.
FT SIGNAL 1 18 PROBABLE.
FT PROPEP 19 24 ACTIVATION PEPTIDE (PROBABLE).
FT CHAIN 25 259 SUBMANDIBULAR/RENAL.
FT FT ACT_SITE 63 63 CHARGE RELAY SYSTEM.
FT ACT_SITE 118 118 CHARGE RELAY SYSTEM.
FT DISULFID 211 211 CHARGE RELAY SYSTEM.
FT DISULFID 31 171 BY SIMILARITY.
FT DISULFID 48 64 BY SIMILARITY.
FT DISULFID 150 217 BY SIMILARITY.
FT DISULFID 182 196 BY SIMILARITY.
FT DISULFID 207 232 BY SIMILARITY.
FT CARBOHYD 91 91 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 106 106 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 259 AA; 28759 MW; 535A8EE25435144F CRC64;

Query Match 40.2%; Score 611.5; DB 1; Length 259;
Best Local Similarity 43.4%; Pred. No. 1.5e-48;
Matches 112; Conservative 45; Mismatches 88; Indels 13; Gaps 3;

QY 36 LQILALATGLVG---GETRIKGFCKPHSQPQALAFKTRLLCGATLIAPRWLT 91
DB 3 LQILFLVLSVRIDAPPGQSRVGVGYCKEKNSQFWQAVI--NRYLGGVLIIDPSWVT 60
QY 92 AAHCLKPRIVHAGNLOKESCEOTRATESFFPRGPN-----NSLPKNDHNDIM 144
DB 61 AAHCSHNVHVLGRNNLFKDEPFAPYRVNOSFPHPDYNPFPMKNTLFPDSDHNDIM 120
QY 145 LVKMASPVITWAVRPLTSSRCVTAAGTSCISGMSGSTSSPOLRLPHTRCANITIIHQ 204
DB 121 LHLSPADITDGVKVIDLPTEBPXVGTCLASGWSSTPLPMEFPDDLCVNNILNSE 180
QY 205 KCENAVPGNITDTMVCASVOEGSKDCQDGGPLVCNOSLOGIISWGDPCATRKPGV 264
DB 181 KCIKHTQVVTDMLCAGLEGGKDCNCNDSSGPILCDGVLOGITSSWSPGGETNRPAL 240
QY 265 YTRKVCXYVDWIDETMKN 282
DB 241 YTRKIFKFTSMIKVEMKEN 258

RESULT 15
KLK3_MOUSE
ID KLK3_MOUSE STANDARD; PRT; 261 AA.
AC P00756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glandular kallikrein K3 precursor (EC 3.4.21.35) (Tissue kallikrein)
GN (MGK-3) (7S nerve growth factor gamma chain) (Gamma-NGF).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=85076169; PubMed=6548955;

```

```

RA Ullrich A., Gray A., Wood W.I., Hayflick J., Seeburg P.H.;
RT "Isolation of a cDNA clone coding for the gamma-subunit of mouse
RT nerve growth factor using a high-stringency selection procedure.";
RL DNA 3:367-392(1984).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE=85257431; PubMed=3848399;
RA Evans B.A., Richards R.I.;
RT "Genes for the alpha and gamma subunits of mouse nerve growth factor
RT are contiguous.";
RL EMBO J. 4:133-138(1985).
RN (3)
RP SEQUENCE OF 25-261.
RX MEDLINE=81264363; PubMed=7263706;
RA Thomas K.A., Baglan N.C., Bradshaw R.A.;
RT "The amino acid sequence of the gamma-subunit of mouse submaxillary
RT gland 7 S nerve growth factor.";
RL J. Biol. Chem. 256:9156-9166(1981).
RN (4)
RP X-RAY CRYSTALLOGRAPHY (3.15 ANGSTROMS) OF 7S COMPLEX.
RC STRAIN=Swiss Webster; TISSUE=Submaxillary gland;
RX MEDLINE=98035451; PubMed=9351801;
RA Bax B., Blundell T.L., Murray-Rust J., McDonald N.O.;
RT "Structure of mouse 7S NGF: a complex of nerve growth factor with
RT four binding proteins.";
RL Structure 5:1275-1295(1997).
CC -1- FUNCTION: 7S NGF ALPHA CHAIN STABILIZES THE 7S COMPLEX. THE BETA
CC DIMER PROMOTES NEURITE GROWTH. THE GAMMA CHAIN IS AN ARGININE-
CC SPECIFIC PROTEASE; IT MAY ALSO HAVE PLASMINOGEN ACTIVATOR
CC ACTIVITY, AS WELL AS MITOGENIC ACTIVITY FOR CHICK EMBRYO
CC FIBROBLASTS.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage of Arg-Xaa bonds in
CC small molecule substrates. Highly selective action to release
CC kallidin (Ilyyl-bradykinin) from kininogen involves hydrolysis of
CC Met-Xaa or Leu-Xaa.
CC -1- SUBUNIT: 7S NERVE GROWTH FACTOR IS COMPOSED OF TWO ALPHA CHAINS,
CC A BETA DIMER COMPOSED OF IDENTICAL CHAINS, AND TWO GAMMA CHAINS.
CC -1- MISCELLANEOUS: THIS PRECURSOR IS CLEAVED INTO SEGMENTS TO PRODUCE
CC THE ACTIVE FORM OF THE GAMMA CHAIN, WHICH OCCURS NATURALLY AS
CC COMBINATIONS OF EITHER TWO OR THREE SEGMENTS HELD TOGETHER BY
CC DISULFIDE BONDS: B1 + A OR B1 + C + B2.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, KALLIKREIN SUBFAMILY.
CC
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CC -----
CC EMBL: X01389; CAA25645.1; -.
CC EMBL: X01798; CAA25928.1; -.
CC EMBL: X01799; CAA25930.1; -.
CC PIR: A91005; NMSG.
CC PDB: 1SGF; 27-MAY-98.
CC MEROPS: S01.170; -.
CC MGD: MGI:97322; Ngfg.
CC InterPro: IPR001254; Ser protease_Try.
CC Pfam: PF00089; trypsin.1.
CC SMART: SM00020; Tryp_Spc.1.
CC PROSITE: PS50240; TRYPSIN_DOM.1.
CC PROSITE: PS00134; TRYPSIN_HIS.1.
CC PROSITE: PS00135; TRYPSIN_SER.1.
CC K01 Hydroxylase; Serine protease; Glycoprotein; Multigene family; Zymogen;
CC Signal; Growth factor; 3D-structure.
FT SIGNAL 1 18 PROBABLE.
FT PROPEP 19 24 ACTIVATION PEPTIDE.
FT CHAIN 25 261 GLANDULAR KALLIKREIN K3.
FT CHAIN 112 107 NERVE GROWTH FACTOR GAMMA CHAIN 1.
FT ACT_SITE 65 65 NERVE GROWTH FACTOR GAMMA CHAIN 2.
FT ACT_SITE 120 120 CHARGE RELAY SYSTEM.

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CHARGE RELAY SYSTEM.

N-LINKED (GLUCNAC. . .).

SEGMENT B1.

SEGMENT A.

SEGMENT C.

SEGMENT B2.

MISSING (IN REF. 2).

FT ACT SITE 213 213

FT DISULFID 31 173

FT DISULFID 50 66

FT DISULFID 152 219

FT DISULFID 184 198

FT DISULFID 209 234

FT CARBOHYD 102 102

FT DOMAIN 25 107

FT DOMAIN 112 261

FT DOMAIN 112 164

FT DOMAIN 165 261

FT CONFLICT 108 111

FT STRAND 26 26

FT STRAND 29 30

FT HELIX 33 35

FT TURN 37 38

FT STRAND 39 44

FT TURN 45 46

FT STRAND 47 56

FT TURN 57 58

FT STRAND 59 62

FT HELIX 64 66

FT STRAND 72 75

FT STRAND 79 79

FT TURN 80 81

FT TURN 85 86

FT STRAND 88 97

FT TURN 99 100

FT HELIX 103 105

FT TURN 118 119

FT STRAND 122 126

FT TURN 148 149

FT STRAND 151 156

FT STRAND 159 159

FT STRAND 167 167

FT STRAND 170 170

FT STRAND 172 179

FT HELIX 181 187

FT TURN 194 195

FT STRAND 196 200

FT STRAND 207 207

FT TURN 210 211

FT TURN 213 214

FT STRAND 216 219

FT TURN 220 221

FT STRAND 222 229

FT TURN 234 235

FT TURN 237 238

FT STRAND 241 245

FT HELIX 246 249

FT HELIX 250 258

FT TURN 259 259

SQ SEQUENCE 261 AA; 28998 MW; 4870748E174AF7C8 CRC64;

Query Match 40.2%; Score 611.5; DB 1; Length 261;

Best Local Similarity 43.0%; Pred. No. 1.5e-48;

Matches 110; Conservative 52; Mismatches 83; Indels 11; Gaps 2;

Qy 38 LILALATGLVGG---ETRIIKGFCKPHSOPWQALFEKTRLLCGATLIPRWLTPAA 93

Db 5 ILFLALSLGIDAAPVQSRIVGGFKCKNSOPMHWAVRYTOYLCGVLLDPNWLTPAA 64

Qy 94 HCLKPRYIVHLGOHNLQKEGCEQTRTATESFPHPGFNNSLPNK-----DHRNDIMLV 146

Db 65 HCYDNDYKWLKGNLKFDEPSAQHRFVSKAIPHPGFNNSLMRKHIRFLEYDYSNDLML 124

Qy 147 KMASPWSITWAVRPLTLSSRCVTAGTSCLSGWSGTSSPOLRLPHTLRCANITIEHOKC 206

Db 125 RLKSKPADIDTVKPIPLPTEEPKLGSTCLASGWSITTPKFQFTDDLVCVNLKLPNEDC 184

Qy 207 ENAYPGNITDTWVCASVQEGKDSGCGSGPLVNCNOSLOGIISWGQDPCATRRKGVYT 266

Db 185 AKAHIEKVTDAULCAGEMDGGKDTCKGDSGGPLICDGVLOGITSMGHTPCGEPDMPGVYT 244

Qy 267 KVCKYVDWIOETMKNN 282

Db 245 KLNKFTSWIKDTMAKN 260

Search completed: October 22, 2003, 15:51:57

Job time : 10.935 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2003, 15:48:57 ; Search time 35.319 Seconds
(without alignments)
2060.389 Million cell updates/sec

Title: US-09-856-320a-2

Perfect score: 1523
Sequence: 1 MORLRLRDMKSSGRGLTAA.....GVYTKVCKYDWIQTMMKN 282

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP archaea: *
2: SP bacteria: *
3: SP fungi: *
4: SP human: *
5: SP invertebrate: *
6: SP mammal: *
7: SP mhc: *
8: SP organelle: *
9: SP phage: *
10: SP plant: *
11: SP rodent: *
12: SP virus: *
13: SP vertebrate: *
14: SP unclassified: *
15: SP viirus: *
16: SP bacteriaph: *
17: SP archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1332.5	87.5	275	4	Q8IXD7
2	1187	77.9	276	11	Q9QYN3
3	1129	74.1	249	11	Q9QYN4
4	692	45.4	260	4	Q8IM69
5	685.5	45.0	255	4	Q96R00
6	683.5	44.9	254	4	Q96R04
7	678	44.5	276	11	Q8CGR6
8	665	43.7	251	11	Q8CGR6
9	632	41.5	293	11	Q9DB08
10	626	39.5	250	11	Q9D140
11	602	39.5	261	11	Q9JMT0
12	600.5	39.4	246	11	Q921R9
13	599.5	39.4	234	11	Q9CV76
14	598.5	39.3	246	11	Q9K077
15	597.5	39.2	239	11	Q63275
16	597	39.2	246	11	Q9QUK9

17	592.5	38.9	261	6	Q9N1Q1	Q9n1q1 saginus oe
18	591.5	38.8	261	6	Q29474	Q29474 canis faml
19	587.5	38.6	235	11	Q63274	Q63274 ratus norv
20	582	38.2	249	11	Q91VE3	Q91ve3 mus musculu
21	576	37.8	263	11	Q9JMT1	Q9jmt1 mus musculu
22	575	37.8	244	13	Q8QGW3	Q8qgw3 anguilla ja
23	572.5	37.6	261	11	Q8C232	Q8c232 mus musculu
24	572	37.6	251	11	Q54854	Q54854 ratus norv
25	570.5	37.5	263	11	Q9JMT6	Q9jmt6 mus musculu
26	570.5	37.5	269	4	Q8IUS5	Q8ius5 homo sapien
27	568.5	37.3	253	11	Q91Y82	Q91y82 mus musculu
28	568	37.3	246	11	Q88301	Q88301 mus musculu
29	567.5	37.3	247	11	Q9CPN7	Q9cpn7 mus musculu
30	567	37.2	240	13	Q98TH0	Q98th0 engraulis j
31	566	37.2	245	13	Q42160	Q42160 petromyzon
32	564.5	37.1	237	13	Q91515	Q91515 tuigu rubrip
33	563	37.0	247	13	Q42158	Q42158 petromyzon
34	562	36.9	247	13	Q42608	Q42608 petromyzon
35	561	36.8	247	11	Q9CPN9	Q9cpn9 mus musculu
36	560.5	36.8	253	4	Q8NSN9	Q8nsn9 homo sapien
37	560	36.8	244	13	Q42159	Q42159 petromyzon
38	559	36.7	242	13	Q92099	Q92099 paratoche
39	558	36.6	254	6	Q9XSN6	Q9xsn6 sus scrofa
40	556	36.5	238	13	Q9W7Q6	Q9w7q6 paratichy
41	555.5	36.5	222	13	Q8AV11	Q8av11 oncorhynch
42	553	36.3	243	13	Q8AV83	Q8av83 brachydant
43	553	36.3	261	11	Q88309	Q88309 mus musculu
44	552	36.2	242	13	Q9W7Q7	Q9w7q7 paratichy
45	551	36.2	247	13	Q9W7Q5	Q9w7q5 paratichy

ALIGNMENTS

RESULT 1
Q8IXD7 PRELIMINARY; PRT; 275 AA.
AC Q8IXD7;
DT 01-MAR-2003 (TRMBLrel. 23, Created)
DT 01-MAR-2003 (TRMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRMBLrel. 23, Last annotation update)
DE Variant form hipostasin/KLK11.
GN KLK11.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N. A.
RC TISSUE=Prostate;
RA Nakamura T., Mitsui S., Miki T., Yamaguchi N.;
RT "Molecular cloning and expression of a variant form of
RT hipostasin/KLK11 in prostate."
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB078780; BACS4105.1; -
SQ SEQUENCE 275 AA; 30165 MW; 257AA42B28F40E2C4 CRC64;

Query Match 87.5%; Score 1332.5; DB 4; Length 275;
Best Local Similarity 90.9%; Pred. No. 3.9e-130;
Matches 250; Conservative 0; Mismatches 0; Indels 25; Gaps 1;
QY 33 MRIDLLILALATGIVGGETRIIKGFCKPHSQPQALFEKTRLLCGATLIAPRWLTA 92
1 MRIDLLILALATGIVGGETRIIKGFCKPHSQPQALFEKTRLLCGATLIAPRWLTA 60
DB 1
QY 93 AHCLKP-----RYIVHLGQNLQKEEGCEQRTATESPFP 127
61 AHCLKPWSLSPPHVSPDLSNNVCLSHLSRIYVHLGQNLQKEEGCEQRTATESPFP 120
DB 61
QY 128 PGFNNSLPNKDRNDIMLVKASPVSTWAVPLTLSSRCVTAGTSCILSGWGSTSPQL 187
121 PGFNNSLPNKDRNDIMLVKASPVSTWAVPLTLSSRCVTAGTSCILSGWGSTSPQL 180
DB 121

QY 188 RLPHLRCAITRIIEHOKENAYPGNITDTWVCASVOEGKSCGDSGGLVNCOSLOG 247
 DB 181 RLPHLRCAITRIIEHOKENAYPGNITDTWVCASVOEGKSCGDSGGLVNCOSLOG 240
 QY 248 IISWGODPCAITRKPGVYTKVCKYVDMIOETMKN 282
 DB 241 IISWGODPCAITRKPGVYTKVCKYVDMIOETMKN 275

RESULT 2

09OYN3 PRELIMINARY; PRT: 276 AA.

AC 09OYN3: 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Hipostasin prostate type.
 GN PRSS20.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RA Yamaguchi N., Mitsui S.;
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RA MEDLINE=20525460; PubMed=11072088;
 RX Mitsui S., Okui A., Komahara K., Uemura H., Yamaguchi N.;
 RT "CDNA cloning and tissue-specific splicing variants of mouse
 RT hipostasin/TPSP (PRSS20).";
 RL Biochim. Biophys. Acta 1494:206-210(2000).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 DR EMBL: AB016227; BAA36955.1; -
 DR HSSP: P00763; IDPO.
 DR MEROPS: S01.257; -
 DR MGD: MGI:1929977; PRSS20.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001254; Ser. protease_Try.
 DR Pfam: PF00089; Trypsin; I.
 DR PRINTS: PR00722; CHYMOTRYPsin.
 DR SMART: SM0020; Tryp_SPC; 1.
 DR PROSITE: PS00240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KM Hydrolyase; Protease; Serine protease.
 SQ SEQUENCE 276 AA; 30753 MW; 90BDC03A8AB178D6 CRC64;

Query Match

Best Local Similarity 77.9%; Score 1187; DB 11; Length 276;
 Matches 217; Conservative 28; Mismatches 31; Indels 6; Gaps 2;

QY 1 WORLDWIDKSSGKGLTAKEPGARSSPLQAMRIQLILALATGLVGGETRIIKGPEC 60
 DB 1 MRLK--SDMKLS---TETREPGRPALIQRMILRLALALVGHVGGETRIIKGYEC 54
 QY 61 KHSQPMQALFEKTRLLCGATLLAPRWLLTAHCLKPRYIYHLOQNLQKEGGEQRT 120
 DB 55 RHSPQWQVALFOKTRLLCGATLLAPRWLLTAHCKRPYVILLGEHMLEKTDGGEORRM 114
 QY 121 ATESPHPGFNNLSLPKDHNDIMLVKASPVSIIMAVPLTLSSRCVTAAGTSCISGMG 180
 DB 115 ATESPHPGFNNLSLPKDHNDIMLVKASPVSIIMAVPLTLSSRCVTAAGTSCISGMG 174
 QY 181 STSSPOLRLPHLRCAITRIIEHOKENAYPGNITDTWVCASVOEGKSCGDSGGLV 240
 DB 175 TSSPOLRLPHLRCAITRIIEHOKENAYPGNITDTWVCASVOEGKSCGDSGGLV 234
 QY 241 CNGSLQGIISWGODPCAITRKPGVYTKVCKYVDMIOETMKN 282

DB 235 CNGSLQGIISWGODPCAITRKPGVYTKVCKYVDMIOETMKN 276

RESULT 3

09OYN4 PRELIMINARY; PRT: 249 AA.

AC 09OYN4: 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE HIPPOSTASIN (2310015108RIK protein).
 GN PRSS20 OR 2310015108RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Yamaguchi N., Mitsui S.;
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Mitsui S., Yamaguchi N.;
 RT "CDNA cloning of a novel brain serine protease, Hipostasin.";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batelov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Stebbins F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carinci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kanaya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli I., Sakamoto N.,
 RA Noriote P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL: AB016226; BAA88825.1; -
 DR EMBL: AK009720; BAB26461.1; -
 DR EMBL: AK009360; BAB26241.1; -
 DR HSSP: P00763; IDPO.
 DR MEROPS: S01.257; -
 DR MGD: MGI:1929977; PRSS20.
 DR InterPro: IPR001254; Ser. protease_Try.
 DR Pfam: PF00089; Trypsin; I.
 DR SMART: SM0020; Tryp_SPC; 1.
 DR PROSITE: PS00240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KM Hydrolyase; Protease; Serine protease.
 SQ SEQUENCE 249 AA; 27604 MW; P9F9CB857D727D5 CRC64;

Query Match

Best Local Similarity 74.1%; Score 1123; DB 11; Length 249;
 Matches 201; Conservative 24; Mismatches 23; Indels 0; Gaps 0;

QY 35 ILQILALATGLVGGETRIIKGPEKPSOPQALFEKTRLLCGATLLAPRWLLTAH 94
 DB 2 ILRLIALALVGHVGGETRIIKGYECRPHSPQWQVALFOKTRLLCGATLLAPRWLLTAH 61

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QY 95 CLKPRYIVHLGOHNLQKEGCEQTRTATESFPHGFNNSLPNKDRNDIMLVKASPVSI 154
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 62 CRPRHYIILGENHLEKTDCCBORRNATESFPHPDFNNSLPNKDRNDIMLVKASSPVFI 121

QY 155 TMAVRPLTLSSRCVTAAGTSCILISGWGSTSSPOLRLPHTLRCAINTIIHOKCENAVPGNI 214
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 122 TRAVQPLTLSPHCVAAGTSCILISGWGSTSSPOLRLPHTLRCAVAVSIIEHKECKAYPGNI 181

QY 215 TDTMVCAVQEGKDCSQGSGGGLVNCOSLOGIISWGDPFCATRKPRGYTTCYKXVDW 274
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 182 TDTMLCAVKEKDKSCQSGSGGLVNCOSLOGIISWGDPFCATRKPRGYTTCYKXVDW 241

QY 275 IOETMKNN 282
   |||:|||||:
DB 242 IHEVMKNN 249

RESULT 4
Q81W69 PRELIMINARY; PRT; 260 AA.
ID 081W69;
AC 081W69;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypochemical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxId=9606;
RN 1)
RP SEQUENCE FROM N.A.
RC Straussberg R.;
RA Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC040887; AA040887.1;
KM Hypochemical protein.
SQ SEQUENCE 260 AA; 28090 MW; EF5934BB96295660 CRC64;

Query Match 45.4%; Score 692; DB 4; Length 260;
Best Local Similarity 49.2%; Pred. No. 1,4e-63;
Matches 125; Conservative 45; Mismatches 80; Indels 4; Gaps 3;

QY 26 RSSPLQAMRLIQLL--ALATGLVGEETRIIKGFCKPHSPQWQALPEKTRTLGATL 83
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 3 RPPRAKKTWPLLLLGAWAGHSRAOEDKVLGHECOPIHSPWQALFQGGQLCGVL 62

QY 84 IAPRWLLTAHCLKPRYIVHLGOHNLQKEGCEQTRTATESFPHGFNNSLPNKDRNDI 143
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 63 VGGNWTUTAHCKKPKYVALGSHSLONKDPPEDEIPVQSIHPPCYNSS-DVEDINHD 121

QY 144 MLVKMASPVSI TMAVRPLTLSSRCVTAAGTSCILISGWGSTSSPOLRLPHTLRCAINTII 203
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 122 MLQLDQSLGSKVRPISLADHCTOPGQKCTVSGMGTVSPRENPDPLNCAEVKIFQ 181

QY 204 QKCNAYPGNITDTMVCAVQEGKDCSQGSGGGLVNCOSLOGIISWGDPFCATRKPR 263
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 182 KKCEDAVPGITDVMVCAVSGSKA-DTCQDSSGGLVNCOSLOGIISWGSDPCGRSDKPG 240

QY 264 VYTKVCKYVDWIOE 277
   |||:|||||:
DB 241 VYTNICRYLDWIKK 254

RESULT 5
Q96R00 PRELIMINARY; PRT; 255 AA.
ID 096R00;
AC 096R00;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Proctinogen.
OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxId=9606;
RN 1)
RP SEQUENCE FROM N.A.
RX MEDLINE=21226193; PubMed=11327827;
RA Takayama T.K., Carter C.A., Deng T.;
RT "Activation of prostate-specific antigen precursor (pro-PSA) by
RT prostin, a novel human prostatic serine protease identified by
RT degenerate PCR.";
RL Biochemistry 40:1679-1687(2001).
CC EMBL; AF303046; AAK62813.1;
DB HSSP; P00761; 1AN1.
DR MEROPS; S01.081;
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001254; Ser_protease_try.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 255 AA; 27986 MW; 00D5B79E14B9468F CRC64;

Query Match 45.0%; Score 685.5; DB 4; Length 255;
Best Local Similarity 49.6%; Pred. No. 6,5e-63;
Matches 129; Conservative 40; Mismatches 76; Indels 15; Gaps 4;

QY 33 MRILQILALATGLVGEETRIIKGFCKPHSPQWQALFEKTRTLGATLAPRWLLTA 92
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MWLLTLSPFLASTAQDGD-KLLEGECAPHQPMQVVALYERGFVCGASLSPHVLVA 59

QY 93 AHCLKPRYIVHLGOHNLQKEGCEQTRTATESFPHGFNNSLPNKDRNDIMLVKASPV 152
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 60 AHQSRFMRVRLGEHNLRRKDPPEQLRTTSRYIHPHRYE---ARSHRDIMLRVOPA 115

QY 153 SITWNRPLTLSSRCVTAAGTSCILISGWGSTS-----SP--QLRPLTLCANTII 202
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 116 RINPQVRPAVLPTRCCHPEACVSGWGLVSHNEPCTAGSPSQVSLPHTLRCAINTG 175

QY 203 HOKCENAVPGNITDTMVCAVQEGKDCSQGSGGGLVNCOSLOGIISWGDPFCATRKPR 262
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 176 DTSQDSYGRGLTNMTMVCAVGAEGRAESCEGSGGLVCGILQGIIVSGDVPDONTTP 235

QY 263 GYTTKVCYVDWIOETMKNN 282
   |||:|||||:|||||:|||||:|||||:|||||:
DB 236 GYTTKVCYLEWIRETMKNN 255

RESULT 6
Q8CGR4 PRELIMINARY; PRT; 254 AA.
ID 08CGR4;
AC 08CGR4;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Proctin.
GN KLK15.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxId=10090;
RN 1)
RP SEQUENCE FROM N.A.
RX MEDLINE=22325484; PubMed=12437987;
RA Olsson A.Y., Lundvall A.;
RT "Organization and evolution of the glandular kallikrein locus in Mus
RT musculus.";
RL Biochem. Biophys. Res. Commun. 299:305-311(2002).
RN 12)
RP SEQUENCE FROM N.A.
RA Adame M., Mural R.;

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RU Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY152434; AAN78422.1; -
 SQ SEQUENCE 254 AA; 28042 MW; AA9E38BEDD01861 CRC64;

Query Match 44.9%; Score 683.5; DB 11; Length 254;
 Best Local Similarity 50.2%; Pred. No. 1e-62;
 Matches 128; Conservative 38; Mismatches 74; Indels 15; Gaps 4;

QY 36 LQILALATGLVGGETRIIKGFECCKPHSQPQALFEKTRLLCGATLIAPRWLLTAHC 95
 DB 3 LLLAFVLVSAADGD-KVLEGECEVPHSQPQALFERGRFNCGAFILSPRWLLTAHC 61
 QY 96 LKPRIVYHGHNLQKEGCEQOTRTATESFPHPGFNNSLPNDRNDIMLVKMASPVST 155
 DB 62 QTRFKVRIRGEHNLRFDPGEQLRSVSRILPHPGYE---ARTHRDMLLRFKPARLT 117
 QY 156 WAWRPPLTSSRCVTAAGTSCGISGWC--STSSP-----QLRLPHTRCANITIIHQK 205
 DB 118 AVRRVAPALPRCPPLIGEDCVSGKGLSDNNFGATGSKSHVRLPDLHCANISIISEAS 177
 QY 206 CENAYPGNITDTMVCASVQEGKDSQGDGSGPLVCNOSLQGIISWGDPCAITRPGVY 265
 DB 178 CNKDYPGRVLPMTMVCAGVGGGTDSCEGSGPLVCGALQGVSGVDVPCDTTKPGVY 237
 QY 266 TVCKYVVDWIOETMK 280
 DB 238 TVCKYLEWIMENVR 252

RESULT 7

QY 08CGR6 PRELIMINARY; PRT; 276 AA.
 AC 08CGR6;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Glandular kallikrein KLK13.
 GN KLK13.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22325484; PubMed12437987;
 RA Olsson A.Y., Lundwall A.;
 RT "Organization and evolution of the glandular kallikrein locus in Mus musculus."
 RL Biochem. Biophys. Res. Commun. 299:305-311(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Adams M., Mural R.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY152432; AAN78420.1; -
 SQ SEQUENCE 276 AA; 30360 MW; 33E189C67492FDC4 CRC64;

Query Match 44.5%; Score 678; DB 11; Length 276;
 Best Local Similarity 47.9%; Pred. No. 4.3e-62;
 Matches 127; Conservative 43; Mismatches 81; Indels 14; Gaps 3;

QY 29 PLQANRIIDLIILALATGLVGGETRIK-----GFECCKPHSQPQALFEKTRRL 77
 DB 3 PLVA--TIACTLTALASEGISRDYPKILNTNGTSGFLPGGYCLPHSQPQALILRGFL 60
 QY 78 LCGATLIAPRWLLTAHCILKPRIVYHGHNLQKEGCEQOTRTATESFPHPGFNNSLPNK 137
 DB 61 LCGGVLVHKKWVLTAAHCKRDKGTVYHGLGHALGRVENGQAMEVYRSTIHPHYQVTPPHL 120
 QY 138 DHRNDIMLVKMASPVSTIWAAPRLTSS-RCVTAAGTSCGISGSGTSSPQLRLPHTLRCA 196
 DB 121 NHDHDMLELKSPPVQLSSHVRLTKLSADDCLPYGCRCVSGWGTTTSPQVNPYPTLQCA 180
 QY 197 NITIEHQKCEANYPGNITDTMVCASVQEGKDSQGDGSGPLVCNOSLQGIISWGDPCC 256

DB 161 NIELSDECEQVYPGKITANMLCAIGTKEGKDSCEGSGPLVCGALQGVSGVDVPCDTTKPGVY 240
 QY 257 AITRKPGVYTVCKYVVDWIOETMK 281
 DB 241 GQPNRPGVYTRVSKYLRWIRRIIRN 265

RESULT 8

QY 09DBQ8 PRELIMINARY; PRT; 251 AA.
 AC 09DBQ8;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE 1200016C12Rik protein.
 GN 1200016C12Rik.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aizawa K., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.W., Stauble F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombereys P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 DR EMBL: AK004807; BAB23579.1; -
 DR HSSP: P00763; IDPO.
 DR MEROPS: S01.307; -
 DR MGD: MGI:1921082; 1200016C12Rik.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR001254; Ser_protease_Try.
 DR Pfam: PF00089; trypsin_1.
 DR PRINTS: PRO0722; CHYMOTRYPSIN.
 DR SMART: SMO0020; Tryp_Spc; 1.
 DR PROSITE: PS00340; TRYPSIN_DOM; 1.
 DR PROSITE: PS00340; TRYPSIN_HIS; 1.
 DR HydroLase: Protease; Serine protease.
 SQ SEQUENCE 251 AA; 28153 MW; FAD667F8C80C4A23 CRC64;

Query Match 43.7%; Score 665; DB 11; Length 251;
 Best Local Similarity 51.0%; Pred. No. 8.7e-61;
 Matches 126; Conservative 40; Mismatches 81; Indels 0; Gaps 0;

QY 36 LQILALATGLVGGETRIIKGFECCKPHSQPQALFEKTRLLCGATLIAPRWLLTAHC 95
 DB 5 LTVLVFSLAHCAGADRRAVARGCVNSXPMQAGFLYLRQLCGATLIINQWLLTAHC 64
 QY 96 LKPRIVYHGHNLQKEGCEQOTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVST 155
 DB 65 RKPVLWVLRGHHLMRWEGPQLLVTDFFPHPGFNNSLNDHNDMDMLIRLPKRVALT 124
 QY 156 WAWRPPLTSSRCVTAAGTSCGISGSGTSSPQLRLPHTLRCANITIIHQKCEANYPGNIT 215

Db 125 PAVQPLNLTESRPVPTQCLIFGMGVSYSKLOYPMTLOCANISILDNKFCRWAYGHIF 184
QY 216 DTWVCAVOEGKDSGCGSGPLVNCOSLOGIISMGODPCATRKRGVYTKCKVDM 275
Db 185 KKLICAGLWEGSGSCGDPGGLVCEGTLAGIVFGFEGPCSRPRPVAITNVFDYLEWI 244
QY 276 QETMKNN 282
Db 245 ESPMERK 251

RESULT 9

Q9D140 PRELIMINARY; PRT; 293 AA.
AC Q9D140; MEDLINE=21085660; PubMed=11217851;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE 110030019R1K protein.
GN 110030019R1K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Embryo;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuenli P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Stabili F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guestinch S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitlaker C., Williams L.,
RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohseki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection."
RT Nature 409:685-690(2001).
CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AK003996; BAB23113.1; -.
DR HSSP; P00763; IDPO.
DR MEROPS; S01.017; -.
DR MEROPS; S01.418; -.
DR MGD; MGI:1915918; 1110030019R1K.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001254; Ser protease_Try.
DR Pfam; PF00089; trypsin_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS00240; TRYP_SIN_DOM; 1.
DR PROSITE; PS00134; TRYP_SIN_HIS; 1.
DR PROSITE; PS00135; TRYP_SIN_SER; 1.
KM Hydroxylase; Serine protease.
SQ SEQUENCE 293 AA; 31908 MW; ED1F45D8226FE911 CRC64;

Query Match 41.5%; Score 632; DB 11; Length 293;
Best Local Similarity 45.8%; Pred. No. 2,8e-57;
Matches 114; Conservative 49; Mismatches 72; Indels 14; Gaps 5;

QY 43 LATGLVGR-----TRIKGFCKPHSQPQQA-LFEKTLILGATLIARPLITAAH 94
Db 50 LSTDSKSGEDTRSDSSSRIVNGSDCKQAPQWQALLLPNKLTCGAVLVISPMWLLTAAH 109

QY 95 CLKPRYIVHAGHNLQK-EEGCEQRTATSEFPHPGPNLSLPNKHNDIMLVKASPV 153
Db 110 CKRPVPRIRLGHNSMSPVYESQGMFGKSLIPHEVS----HFGSNLMLIKMKRKIR 165
QY 154 ITWAVRPLTLSSRCVTAGTSCILSGWSTSSPOLRPLHTLRCAITIIIEHOKENY 213
Db 166 DSHSVKPEIACDCATEGTRCMVSGWGTSSSHNNPFPVLCINTIVLSEERCKNYS 225
QY 214 ITDTWVCAVOEGKDSGCGSGPLVNCOSLOGIISMGODPCATRKRGVYTKCKYVD 273
Db 226 IOKTWFCADEE-GRDSCGDSGSPVNCGLQGLVSWGDFPCAQRNRPBGVYTNLCEPVK 284
QY 274 WIOETMKNN 282
Db 285 WIKDTMNSN 293

RESULT 10

Q8CGR5 PRELIMINARY; PRT; 250 AA.
AC Q8CGR5; MEDLINE=22325484; PubMed=12437987;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Glandular kallikrein KLK14.
GN KLK14.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22325484; PubMed=12437987;
RA Olsson A.Y., Lundwall A.,
RT "Organization and evolution of the glandular kallikrein locus in Mus
RL Biochem. Biophys. Res. Commun. 299:305-311(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Adams M., Mural R.,
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY152433; AAN78421.1; -.
SQ SEQUENCE 250 AA; 27016 MW; F62FEBF2290FEBB8 CRC64;

Query Match 41.1%; Score 626; DB 11; Length 250;
Best Local Similarity 46.1%; Pred. No. 9,8e-57;
Matches 117; Conservative 43; Mismatches 86; Indels 8; Gaps 3;

QY 33 MRILILILATATGLV--GGERRIIKGFCKPHSQPQQA-LFEKTLILGATLIARPW 88
Db 1 MFLDILILQALVAIAQSGQGDHKLITGYRCVANSQPMVOVALAGGHRFLCGVLISDQW 60
QY 89 LTTAAHCLKPRYIVHAGHNLQK-EEGCEQRTATSEFPHPGPNLSLPNKHNDIMLVK 148
Db 61 VITAHCARPLIHVALGHNIRRMWATQGVRAQVHHPOQ----FOAHNDIMLKL 116
QY 149 ASPVSTWAVRPLTLSSRCVTAGTSCILSGWSTSSPOLRPLHTLRCAITIIIEHOKEN 208
Db 117 QKTVLGRAVNTISVASSCASPGTRCVSGWGTIASPIARVPTALQCVVNVINSQACHR 176
QY 209 AVPGWITDTWVCAVOEGKDSGCGSGPLVNCOSLOGIISMGODPCATRKRGVYTKV 268
Db 177 AVPGIITSGWVCAVPEBGKDSGCGSGPLVCGQLGLVSWGMRCAIPGVYANLV 236
QY 269 CKYVDMIOETMKNN 282
Db 237 CNVHSWIRTWQSN 250

RESULT 11
Q9JMW70 PRELIMINARY; PRT; 261 AA.

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AC 09J070;
BT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Glandular kallikrein 21 (Similar to kallikrein 21).
GN KLK21 OR GK21.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20534760; PubMed=11082197;
RA Matsui H., Moriyama A., Takahashi T.;
RT "Cloning and characterization of mouse Klk27, a novel tissue
RT kallikrein expressed in testicular Leydig cells and exhibiting
RT chymotrypsin-like specificity."
RU Eur. J. Biochem. 267:6858-6865(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Salivary gland;
RA Strausberg R.;
RT Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB039276; BAA92319.1; -
DR EMBL: BC012243; AAH12243.1; -
DR HSSP: P00757; 1SGF.
DR MEROPS: S01.038; -
DR MGD: MGI:892022; Klk21.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00089; trypsin; 1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Protease; Serine protease.
SQ SEQUENCE 261 AA; 28690 MW; 608B976BC78E03EE CRC64;

Query Match 39.5%; Score 602; DB 11; Length 261;
Best Local Similarity 42.5%; Pred. No. 3.2e-54;
Matches 111; Conservative 51; Mismatches 87; Indels 12; Gaps 3;

QY 33 MRLILALATGAVG---ETRIIKFECKPHSQPWQAALFEKTRLLCGATLIAPRW 88
DB 1 MRFLLTLFLALSLGEIDAAPVQSRTVGGFNCCKSQSPWHAVALFRNKYICGCVLNPW 59
QY 89 LTTAAHCLKRYIVHLGQNLQKEGCEQTRTATESFPHPGFNNSL-----PNKDHKN 141
DB 60 VLTAAHCVGNQYVNLGKXKLLFQHSSAQHRLVSKSFPHPDVNMGLMNDHTPHREDVSN 119
QY 142 DIMLVKMASPVSIITWAVRPLTSSRCVTAGTSCGISGWSSTSSPOLRLPHLTRCANITII 201
DB 120 DLMRLRSKPADITPAVKPIDLPTEBPKLGSYCLASGWSITPTPKQIIPNDLQCGFIRPL 179
QY 202 EHOKENAVPGNITPTMVCASVOEGGKDSCGDGGPLVCNOSLGGIISWGDDPCAIRK 261
DB 180 PNEACAIAIHKVTDVMLCAGEMGGKDTCADSGGGLCDGVLGITISWGISIPCAKRNA 239
QY 262 PGVYTKVCKYVDMIQETMKN 282
DB 240 PAIYTKLIKFTSMIKDTMAKN 260

RESULT 12
Q9ZIR9 PRELIMINARY; PRT; 246 AA.
AC Q9ZIR9;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DE TRYPSINogen 16.
GN TRYCN16 OR TRYPSINOGEN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Balb/c;
RA Rowen L., Hood L.;
RT "Comparison between strains Balb/c and 129 in a region of the mouse T
RT cell receptor beta locus."
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/c;
RA Chen F., Rowen L., Hood L., Rothenberg E.V.;
RT "Differential transcriptional regulation of individual TCR Vbeta
RT segments before gene rearrangement."
RL J. Immunol. 166:1771-1780(2001).
CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL: AF107342; AAC79093.1; -
DR EMBL: AE000665; AAB69088.1; -
DR HSSP: P00763; 1DPO.
DR MEROPS: S01.063; -
DR MGD: MGI:2148749; Trypnl6.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR001254; Ser_protease_Try.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; Tryp_SPC; 1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Protease; Serine protease.
SQ SEQUENCE 246 AA; 26134 MW; 34E173B18CA2FA63 CRC64;

Query Match 39.4%; Score 600.5; DB 11; Length 246;
Best Local Similarity 47.4%; Pred. No. 4.3e-54;
Matches 120; Conservative 38; Mismatches 88; Indels 7; Gaps 4;

QY 30 LQMRILQILALATGIVGETRIIKFECKPHSQPWQAALFEKTRLLCGATLIAPRW 89
DB 1 MSALLFLVAGAAVAFV-DVDDDKIVGGYTERNSVPQVSL-NSGYHFCGSLINDQMV 58
QY 90 LTAHCLKRYIVHLGQNLQKEGCEQTRTATESFPHPGFNNSLPPNKDHNDIMLVGMA 149
DB 59 VSAHCKYKTRIQVRLGEGHNIVLGENDFIDAAKIYHPPNKRKTLN---NDIMLILKS 114
QY 150 SPVSIITWAVRPLTSSRCVTAGTSCGISGWSSTSSPOLRLPHLTRCANITIIEHOKENA 209
DB 115 SPVTLNARVALPSSCAPAGTQCLISGWKNTISFGVSEEDLQCIDAPLLPQADCEAS 174
QY 210 YPGNITPTMVCASVOEGGKDSCGDGGPLVCNOSLGGIISWGDDPCAIRKPGVYTKVC 269
DB 175 YPGKITGNMVCAGFLEGKDSQCGDGGPVVNCNGLGIVSWGYG-CALPNNPGVYTKVC 233
QY 270 KYVDMIQETMKN 282
DB 234 NYVDMIQDTIAAN 246

RESULT 13
Q9CV76 PRELIMINARY; PRT; 234 AA.
AC Q9CV76;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE 2310008B01RIK protein (Fragment).
GN 2310008B01RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=21085660; Pubmed=11217851;
RA Kawai T., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Atakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schiri L.M., Staahl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli U., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
RA Wyszew-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AK009217; BAB26143.1; -
DR HSSP; P00763; IDPO.
DR MEROPS; S01.020; -.
DR MGD; MGI:1916761; 2310008B01Rik.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Hydrolase; Protease; Serine protease.
KW NON TER
FT SEQUENCE 234 AA; 25888 MW; 6D81E609EDD39110 CRC64;

Query Match 39.4%; Score 599.5; DB 11; Length 234;
Best Local Similarity 46.8%; Pred. No. 5,1e-54;
Matches 108; Conservative 40; Mismatches 78; Indels 5; Gaps 4;

QY 53 RIHKGECKPHSQPQALPEKTRLLCGATLLAPRWLLTAHCLKRYIVHGOHLQOE 112
DB 8 KLYNGECVKNSSQPVQGLFHGKRYLGGVLDVRKWLTAAC-RDKYVVRGESHSLTL 66
QY 113 EGCEQRTATSEFPHPGFNNSLPNKDRNDIMLVKMASPVSIITWAVRPLTLSSRCTACT 172
DB 67 DWTEQQRHHTFTSTHSYQAYON--HEHDLRLRLNRPHILTRAVRPALSSCVTTGA 124
QY 173 SCLISGWSGTSFQRLPHTLRCAITTEIEHOKCENAYGNITDTWVCASVQEGKDSQ 232
DB 125 MGHVSGMGTNNKWDPEPRLQCLNISTVSNETCRAVFGRAVENMLCAG-GEAGKDAQ 183
QY 233 GDSGGLVNGSLGGIISWGQ-DPCAITRKPGYTVCKYVVMIOGTMKN 282
DB 184 GDSGGLVNGSLGGIISWGQ-DPCAITRKPGYTVCKYVVMIOGTMKN 234

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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129SVJ;
RX MEDLINE=99436155; Pubmed=10506205;
RA Ohmura K., Kohno N., Kobayashi Y., Yamagata K., Sato S.,
RA Kashiwabara S., Baba T.;
RT "A homologue of pancreatic trypsin is localized in the acrosome of
RT mammalian sperm and is released during acrosome reaction.";
RL J. Biol. Chem. 274:29426-29432(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Stomach, and Spleen;
RX MEDLINE=21085660; Pubmed=11217851;
RA Kawai T., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Atakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schiri L.M., Staahl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli U., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
RA Wyszew-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RX MEDLINE=21103195; Pubmed=11160223;
RA Chen F., Rowen L., Hood L., Rothenberg E.V.;
RT "Differential transcriptional regulation of individual TCR Vbeta
RT segments before gene rearrangement.";
RL J. Immunol. 166:1771-1780(2001).
CC -i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AB017032; BAA74761.1; -
DR EMBL; AK008667; BAB25821.1; -
DR EMBL; AK003064; BAB25242.1; -
DR EMBL; AE000664; AAB69056.1; -
DR HSSP; P00763; ISLU.
DR MEROPS; S01.057; -.
DR MGD; MGI:1913350; 0910001B19Rik.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Hydrolase; Protease; Serine protease.
KW NON TER
FT SEQUENCE 246 AA; 26274 MW; B6A9FAC99079633F CRC64;

Query Match 39.3%; Score 598.5; DB 11; Length 246;
Best Local Similarity 46.6%; Pred. No. 6.9e-54;
Matches 118; Conservative 41; Mismatches 87; Indels 7; Gaps 4;

QY 30 LQAMRILOLILATLGTGVEGTRIRKGECKPHSQPQALFEKTRLLCGATLLAPRWL 89
DB 1 MRALLFLVGVAAVFP-VDDDKLVGTYTCRENSVPQVSL-NSGYHFCGSLINDQMV 58
QY 90 LTAHCLKPRYIVHGOHLQOECEQRTATSEFPHPGFNNSLPNKDRNDIMLVKMA 149
DB 59 VSAHCVKSYRIQVRGHNINVLGEGNFOVNSAKIKHPNNSRTL----NDIMLIKLA 114

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: October 23, 2003, 15:36:10 ; Search time 2423.21 Seconds
(without alignments)
2828.419 Million cell updates/sec

Title: US-09-856-320A-2
Perfect score: 1523
Sequence: 1 MQRRLRWLRDMKSSGRGLTAA.....GYTVKVCYVDWIQETMKUN 282

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame-p2n.model -DRV=xih
-Q/cgn2_1/USPTO.spool/US09856320/runat_22102003_121415_25672/app_query.fasta_1.846
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-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCCALIGN=200 -THR SCORE=pcst -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCL
-OUTFMT=PCO -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09856320.@CCN_1_1_3596.@runat_22102003_121415_25672 -NCPU=6 -ICPU=3
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
EST:*
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2: em_estchum:*
3: em_estcin:*
4: em_estcmu:*
5: em_estcov:*
6: em_estcpl:*
7: em_estcto:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estom:*
16: em_estfun:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pin:*
20: em_gss_vrt:*
21: em_gss_fut:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_tod:*
26: em_gss_phg:*
27: em_gss_vr1:*
28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1488.5	97.7	1294	11	BC015551 Homo sapi
2	1377.5	90.4	1072	12	BM559782 AGENCOURT
3	1326.5	87.1	1074	12	BM559617 AGENCOURT
4	1284	85.0	853	10	BG720793 602692015
5	1187	77.9	1295	11	AK009360 Mus muscu
6	1187	77.9	1295	11	AK009720 Mus muscu
7	1161	76.2	1269	11	AK009659 Mus muscu
8	1158	75.2	841	12	B1818697 603037514
9	1146	75.2	678	12	B1763040 603047836
10	1110	72.9	708	10	BC697071 602660281
11	1021	67.0	973	10	BE867930 601443517
12	975	64.0	639	10	BG747134 602704354
13	816	53.6	539	12	BM837078 K-EST0113
14	794	52.1	579	12	B1046611 MR3-FN020
15	780	51.2	761	12	BM982377 UI-CF-EN1
16	775	50.9	528	4	BX528424 RZPD Mus
17	744.5	48.9	747	13	BX109836 BX109836
18	724	47.5	467	9	A1893370 mJ99H09.Y
19	723.5	47.5	966	14	BY709314 BY709314
20	720	47.3	467	9	AA073833 mJ99H09.X
21	692.5	45.5	898	14	CB204935 AGENCOURT
22	690.5	45.3	880	14	CB202840 AGENCOURT
23	687	45.1	526	10	BE898804 601681783
24	685	45.0	809	10	BF679282 602153475
25	678.5	44.6	852	14	CB587168 AGENCOURT
26	669	43.9	1048	11	AK004807 Mus muscu
27	653.5	42.9	826	14	CB574882 AGENCOURT
28	640	42.0	484	14	CB270157 Mus muscu
29	632	41.5	1240	11	AK003996 Mus muscu
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31	620.5	40.7	368	9	AA412318 zt97c06.X
32	617	40.5	754	12	B1653899 603280742
33	613	40.2	765	13	EX079152 BX079152
34	613	40.2	766	13	BU416879 603670939
35	613	40.2	808	13	BU416510 603670980
36	613	40.2	857	13	EX078781 BX078781
37	612	40.2	834	13	BU487089 603972168
38	610	40.1	750	13	BU492376 604130628
39	610	40.1	783	13	BU417086 603671080
40	610	40.1	786	13	BU417396 603670539
41	610	40.1	800	13	BU417373 603671011
42	610	40.1	806	13	BU416343 603671007
43	610	40.1	816	13	BU417211 603671638
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ALIGNMENTS

RESULT 1
LOCUS BC015551 1294 bp mRNA linear HTC 29-OCT-2001
DEFINITION Homo sapiens, kallikrein 11, clone IMAGE:3847565, mRNA.
ACCESSION BC015551
VERSION BC015551.1 GI:15930236
KEYWORDS HTC
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1294)
AUTHORS Strausberg,R.

Direct Submission
Submitted (01-OCT-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT	Contact: MGC help desk

Email: cgababos-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www.simg.stanford.edu>
Contact: (Dickson, Mark) med@pdxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRxk Plate: 20 Row: 1 Column: 12
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA y1: 8574338
This clone has the following problem: frame shifted.

FEATURES	Location/Qualifiers
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ORIGIN

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Percent Similarity:	99.308
Best Local Similarity:	98.948
Query Match:	97.73%
BB:	11
Length:	129
Matches:	281
Conservative:	1
Mismatches:	0
Indels:	2
Gaps:	1

US-09-856-320A-2 (1-282) x BC015551 (1-1294)

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Db	179	AAGGAACCTGGGGCCCCGCTCTCCCCCTCCAGGCCATGAGGATTCTGCATTATATCTG	238
Qy	41	LeuAlaLeuAlaThrGlyLeuValGlyGlyIuThrArgIleIleLYSGIYPheGlyCys	60
Db	239	CTTGCTCTGGCAACAGGCGCTTGAGGGGAGAGACAGAGATCATCAAGGGTTGGAGTGC	298
Qy	61	LysProHisSerGlnProTrpGlnAlaIleAlaLeuPheGlyLysThrArgLeuLeuCysGly	80
Db	299	AACCCCTACCTCCAGCCCTTGAGGAGGAGCCCTGTTCAGAAAGCCGGCTACTGTGGG	358
Qy	81	AlaThrLeuIleAlaProArgTrbLeuLeuThrAlaAlaHisCysLeuLysPro----Ar	99
Db	359	GGCAGCGTATGCGCCCCGAGATGGCTCTGACAGAGAGCCCACTGCTTAAGCCGTGGCG	418
Qy	99	GTYrIleValHisLeuGlyGlnHisAsnLeuGlnLysGlyGlnGlyCysGlyGlnThrAr	119
Db	419	CTACATAGTTCAACCTGGGCGACACACACTCCAGAAAGGAGGGGCTGTGACGAGACCG	478
Qy	119	GhrIraIatThrGlySerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHi	139

Db	479	GACAGCAGT	AGTCTTCTCCCAACCCGGCTTCACACAGCCTCCCAACAAAGACA	538
Qy	139	sArGaNaSp11eMeLLeuAlaLyMeCa1ASePrOva1SeR11eThrTrpAlaValAr		155
Db	539	CCGCATGACATCATCATGCTGTGTGAAGATGGCATGCCAGTCTCCATCACCTGGGCTGTGGC		598
Qy	159	gPrOleuThr1LeuSeRSeRArgCyVal1ThAlaG1YThSeRcYs1Leu11eSeRg1YTr		179
Db	599	ACCCCTACCCCTCTCTCTACCGCTGTGTACTGCTGGACACAGCTGCTCATTTCTCCGCTG		658
Qy	179	pG1SeThRSeRSeRSeRProG1nLeuArG1LeuProH1eThrLeuArGcYsAlaLeu11eTh		199
Db	659	GGGAGACAGCTCCAGCCCCCACTTACGCTGTGCTTCACACCTTGGAGTGGCCAAACATCAC		718
Qy	199	r11e11eG1nH1sG1nLyScYsG1uAsna1ATyPrOg1Yasn11eThRAspThRMeVa		219
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Db	779	GTGTGCACACCGCGAGGAAGGGGCGAAGACTCTCTCCAGGGTATCTCCGGGGCCCTCT		838
Qy	239	uValCYsAeNg1nSeRLeuG1nG1Y11e11eSeRTrpG1yG1nAspProCYsAla11eTh		259
Db	839	GGCTGTAAACAGTCTCTTCAAGGATTAATCTCTGGGGCCAGATCCGTGTGCAATCAC		898
Qy	259	rArG1ySPrOg1yAla1YTrThR1ySeVa1CYs1eSTyTrValAspTrp11eG1nG1uThRMe		279
Db	899	CCGAAAGCTGTGTCTACACGAAAGTCTGCAAAATATGTGACTGATGATCCAGAGAGCAT		958
Qy	279	tLySaenAen	282	
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RESULT 2
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LOCUS
DEFINITION
    BMS59782
    AGENCOURT_6565460 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:574441
    5', mRNA sequence.
ACCESSION
    BMS59782
VERSION
    BMS59782.1
KEYWORDS
    GI:18803655
SOURCE
    EST.
ORGANISM
    Homo sapiens (human)
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
    1 (bases 1 to 1072)
AUTHORS
    NIH-MGC http://mgc.nci.nih.gov/.
TITLE
    National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
    Unpublished
COMMENT
    Contact: Robert Strausberg, Ph.D.
    Email: cgabs-remail.nih.gov
    Tissue Procurement: Life Technologies, Inc.
    cDNA Library Preparation: Life Technologies, Inc.
    cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
    DNA Sequencing by: Agencourt Bioscience Corporation
    Clone distribution: MGC clone distribution information can be
    found through the I.M.A.G.E. Consortium/LNL at:
    http://image.llnl.gov
    Plate: LLM12765 row: 1 column: 11
    High quality sequence stop: 684.
FEATURES
    location/Qualifiers
    1..1072

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FEATURES
source
    Location/Qualifiers
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    /note="Organ: brain; Vector: pcwv-SPORT6; Site_1: NoCI;
    Site_2: EcoRV (destroyed); RNA source normal medulla from

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anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH-MGC library."

BASE COUNT 238 a 340 c 307 g 185 t 2 others

ALIGNMENT SCORES:

Pred. No.: 3.9e-117 Length: 1072
Score: 1377.50 Matches: 265
Percent Similarity: 96.39% Conservative: 2
Best Local Similarity: 95.67% Mismatches: 7
Query Match: 90.45% Indels: 3
DB: 12 Gaps: 1

US-09-856-320A-2 (1-282) x BM559782 (1-1072)

QY 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyValArgGlyLeuThrAlaAla 20
DB 116 ATGCAAGATTGAGGTGGGAGTGGAGTGAAGTCAAGGAGGCTCTCACAGACGCC 175
QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleLeu 40
DB 176 AAGGAACCTGGGGCCGCTCTCCCTCCAGGCCATGAGATTCTGCAGTTAATCCTG 235
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyLeuThrArgIleIleLysGlyPheGluCys 60
DB 236 CTTCCTCTGGCAACAGGGCTTGTAGGGGGAGAACACAGGATCTCAAGGGGTTGAGTGC 295
QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlnLysThrArgLeuLeuCysGly 80
DB 296 AAGCCCTCATCCAGCCCTGGCAGGAGCCCTTTGAGAAAGCGGCTACTCTTGGG 355
QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTy 100
DB 356 GCGAGCCTCATGCCCCCAGATGGCTCCGACAGCAGCCACCTGCTCAAGCCCGCTAC 415
QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlyGlyCysGluGlnThrArgThr 120
DB 416 ATGTGTACCTGGGGGAGCACAACCTCCAGAAAGAGAGGGCTGTGACAGACCCGAGCA 475
QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
DB 476 GCCACTGAGCTCTTCCCAAGCCCGGCTTCAACAGAGCTCCCAACAAAGCCACGCCG 535
QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
DB 536 AATGACATCATGCTGTGTAAGATGGCATGCCAGTCTTCATCATCCTGNGCTGTGCAACC 595
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DB 596 CTCACCTCTCCCAAGCTGTGTGCTGCTGAGGACAGCTGCTATTTCCGGCTGGGG 655
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DB 656 AGCAGCTCAGGCCCCAGTTAGCCTGCTCACACCTTCGATGCGCCCAACATCACCATC 715
QY 201 IleGlnHisGlnLysCysGlnAsnAlaTyProGlyAsnIleThrAspThrMetValCys 220
DB 716 ATTGAGCACAAGAGTGTAGAAAGCCTTACCCCGGCAATCATACAGACACCATGGTGT 775
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QY 260 GlySerProGlyValTyThr---LysValCysLysTyVal-AspTrp 274

DB 896 GAAAGCCTGTGTGCTATCCCGAAGGCTCGCAATATGTGGAGCTGG 942

RESULT 3
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AGENCY GenBank 656456 NIH-MGC_119 Homo sapiens cDNA clone IMAGE:5744314
5' mRNA sequence.
ACCESSION BM559617
VERSION BM559617.1 GI:18803348
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1074)
NIH-MGC <http://mgc.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabs-rc@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM12765 row: h column: 11
High quality sequence stop: 689.
Location/Qualifiers
1. 1074
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Site: 2. EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 013. Note:
this is a NIH-MGC library."

FEATURES

source

BASE COUNT 238 a 339 c 311 g 184 t 2 others

ALIGNMENT SCORES:

Pred. No.: 2.06e-112 Length: 1074
Score: 1326.50 Matches: 265
Percent Similarity: 93.71% Conservative: 3
Best Local Similarity: 92.66% Mismatches: 12
Query Match: 87.10% Indels: 6
DB: 12 Gaps: 1

US-09-856-320A-2 (1-282) x BM559617 (1-1074)

QY 1 MetGlnArgLeuArgTrpLeuArgAspTrpLysSerSerGlyValArgGlyLeuThrAlaAla 20
DB 115 ATGCAAGATTGAGGTGGGAGTGGAGTGAAGTCAAGGAGGCTCTCACAGACGCC 174
QY 21 LysGluProGlyAlaArgSerSerProLeuGlnAlaMetArgIleLeuGlnLeuIleLeu 40
DB 175 AAGGAACCTGGGGCCGCTCTCCCTCCAGGCCATGAGATTCTGCAGTTAATCCTG 234
QY 41 LeuAlaLeuAlaThrGlyLeuValGlyGlyLeuThrArgIleIleLysGlyPheGluCys 60
DB 235 CTTCCTCTGGCAACAGGGCTTGTAGGGGGAGAGAACAGATCATCAAGGGGTTGAGTGC 294

OY	61	lysprhohissersglnprotrfglnlalaileuphegiulvsthrargleuencysgily	80
Db	295	aaagctcatctccagaccctggagagagccctgttcgamaacagcggtactctgtggg	354
OY	81	alathrlleuilealaprohgrtrpleuenuthrallahisCysleuylsProArgTyr	100
Db	355	ggcagcgtcatatcgcccccagatggctctgcagacagaccctcctgaagcccgctac	414
OY	101	llevalhislenglyglhnihsasnleuglnlysgliuglycyegliuglthrargthr	120
Db	415	atagttcactctggggcagacacaaCCTCCAGAAAGGAGGAGGCTGTGAGCAGACCGGACA	474
OY	121	AlaThrIuserPheProHisProGlyPheAAsnserLeuProAsnlysaPhisArg	140
Db	475	gccactgagctcttccccaccccccgcttcaacaacagcttcccAACAACAACACCGC	534
OY	141	AsnAspIleMetLeuVallysmetAlaserProValserIleThrTrpAlavalArgPro	160
Db	535	AATGACATCATGCTGGTGAAGATGGCATGCGCAGTCTCATACCTGGGCTGTGGACCC	594
OY	161	LeuthrlseuserSerArgCysValthrIaaglythrserCysleuIleserGlyTrpGly	180
Db	595	ctcaccctctctctcACGCTGTGTCACTGCTGGCACAGCTGCTCATTTCCGGCTGGGGC	654
OY	181	SerThrserSerProGlnleuArgleuprohisThrleuArgCysAlaAsnIleThrIle	200
Db	655	AGCAGCTCCAGCCCCCAGTTAGCCTGCTCACACTTGGCGATGGCCAAACATCACATC	714
OY	201	IleglnHisglnLysCysgluAsnAlaTyrProGlyAsnIleThAspThrMetValCys	220
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OY	221	AlaserValglnIuglyGlyLysaspserysginglyaspSer-GlyGlyProleuVala	240
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OY	240	lCysasnGlnserLeuglnIuglyIleIleserTrp-GlyGlnAspProCys-AlaIleThr	259
Db	835	CTGTATCCAGCTCTCTTCAAGGATTTATCTCCGGGGGGCAGATCCGTGTCGATCAC	894
OY	260	ArgLys-ProGlyValTyrThrLysValCysIleStryVal---AspTrpIle-GlnGluT	278
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LOCUS			
DEFINITION			602692015Fr1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4824387 5',
ACCESSION			mRNA sequence.
VERSION			Bg720793
KEYWORDS			Bg720793.1 GI:13999980
SOURCE			EST.
ORGANISM			Homo sapiens (human)
REFERENCE			Homo sapiens
AUTHORS			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE			Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
JOURNAL			1 (bases 1 to 853)
COMMENT			NIH-MGC http://mgs.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished Contact: Robert Strausberg, Ph.D. Email: cgapbs-rt@mail.nih.gov Tissue Procurement: Miklos Palkovits, M.D., Ph.D. cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiroki Toshiyuki and Piero Carninci (RIKEN) cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:

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http://image.lanl.gov
Plate: L1AM0735 row: n column: 04
High quality sequence stop: 826.
Location/Qualifiers
1. 853

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); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',
size-selected for average insert size 2.2 kb and
normalized to R07 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT
ORIGIN
180 a      285 c      227 g      161 t

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Alignment Scores:	
Pred. No.:	1,48e-109
Score:	129.44
Percent Similarity:	98.42%
Best Local Similarity:	98.02%
Query Match:	84.96%
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Length:	853
Matches:	248
Conservative:	1
Mismatches:	3
Indels:	0
Gaps:	2

US-09-856-320A-2 (1-282) x BG720793 (1-853)

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QY	41	LEUALALEUALATHG1YLEUVALG1YGLIUTHARG1LEILEYSG1YPHGLUCYS	60
Db	157	CTTGCTCTGGCAACAGGGCTGTGAGGGGAGAGACAGAGATCATCAAGGGGTTCGAATGC	216
QY	61	LYSPROHISERG1HPROTPG1NALALEUPHEGLUYSTHARGLEULEUCYSGLY	80
Db	217	AAGCCCATCCACCCCTGGCAGGACACCTGTTCCGAGAAGCGCGCTACTCTGGGG	276
QY	81	ALATHLEUL1A1A1PROARGTPLEULEUHP1AL1A1H1SYSLYU1SPROARGTYR	100
Db	277	GGCACCCTATGCCCCCAGATGCTCTGACACAGCCCATGCTCTCAAGCCCCGGTAC	336
QY	101	ILEVALHISLEUG1YGLNHISASNLEUG1INYSGLUGUG1CYSG1UG1INTHARG1THR	120
Db	337	ATPAGTTACCTGGGACAGACACACTCCAGAAGAGAGGGCTGTGACAGACCCGGACA	356
QY	121	ALATHGLUSERPHEPROHISEROC1YDHEASNA1SERLEUPROAEN1YASPHISARG	140
Db	397	GCCACTGAGTCTTCCCCCAGCCCGGCTTCAACAACAGCCTCCCAACAAGACACACGC	456
QY	141	ASNA1SP1L1MELEULEUVAL1Y1MECAL1A1SERPROVAL1SER1LEH1TRTPAL1AVALARGPRO	160
Db	457	AAGACATCATCTGCTGTAAGATGGCAATCGGCATCTTCATCACCTGGCGTGGCACCC	516
QY	161	LEU1THLEUSERSERARGCYVAL1THR1AG1YH1SERCYSLYU1LE1SERG1YTPRG1Y	180
Db	517	CTCACCCCTCTCTCACCGCTGTCTCACTGCTGGACCAAGCTCCTCATTTCCGGCTGGGGC	576
QY	181	SER1THSER1SER1PROG1L1LEUARGLEUPROHIS1THR1LEUARGCY1A1ASN1LE1THR1LE	200
Db	577	AGCAGCTCCAGCCCCCAGTTAGCGCTGCCTCACACCTTGAGATCGCCCAACATCACATC	636
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Oy	260	gLyspProGlyValYrThrlyValCyslysrVal	272
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DEFINITION			linear HTC 05-DEC-2002
			Mus musculus adult male tongue cDNA, RIKEN full-length enriched
			library, clone:2310015108 product:protease, serine, 20, full insert
			sequence.
ACCESSION	AK009360		
VERSION	AK009360.1	GI:12844110	
KEYWORDS			HTC; CAP trapper.
SOURCE			Mus musculus (house mouse)
ORGANISM			Mus musculus
			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
			Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
PUBMED			
REFERENCE			
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REFERENCE	TITLE	JOURNAL	AUTHORS
5	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.	Nature 409 (6821), 685-690 (2001)	Atakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Himamoto,K., Hirakawa,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kikukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Seno,H., Saeki,D., Shibata,K., Shibata,Y., Shingawa,A., Shitaki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takanashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
6	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs	Nature 420, 563-573 (2002)	6 (bases 1 to 1295)
7	Submitted (10-JUL-2000)	Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gs.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)	
8	Direct Submission		
9	Further details.		
10	CNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.		
11	Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGATCGATCCAGAGCTCTTTTCTTTTCTTTVN 3']. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATTCGAGTATTAAATTAATCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI, 3' end: SstI.		
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13	Location/Qualifiers		
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23	/tissue="tongue"		
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28	putative"		
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33	/translation="MRRLSDWKLSTREPCGAPALLQARNILRLIALVTGVHGGERRIIGYECRPHSQPQWALFOKRLTLCGATLIPKMLITTAHGRKPPYVILIGHNLEKTDQCEBMAATESFPHLPDNNNSLPNDKHNNDIMLVKSSPVFTFAVQPLTSPHCVAAAGSCSLISGCGTSSPOLRLPSLRANVSIIEHKCEKAYAGNITDMLCASVRKEGKSCGDSGGLVCNCSLOGIITISWQDPCAVTRKRPVYTRKCKYFRNHHVNRNN"		
34	polya_signal		
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 Best Local Similarity: 76.95% Mismatches: 31
 Query Match: 77.94% Indels: 6
 DB: 11 Gaps: 2

US-09-856-320A-2 (1-282) x AK009360 (1-1295)

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QY 1 MetGlnArgLeuArgTrpLeuArgSerProLeuArgGlyLeuThrAlaAla 20
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QY 21 LysGluProGlyAlaArgSerProLeuGlnAlaMetArgIleLeuGlnLeuIleu 40
DB 186 AGGGAACCTGGCGCCGCCCTCCCTACTCCAGGCCAGGATATTCTCCGACTCATTTGCA 245
QY 41 LeuAlaIleAlaThrGlyLeuValGlyGlyIleThrArgIleIleLysGlyPheGlyCys 60
DB 246 CTTCCTCTGTGTACAGGGCAGCGATGAGGGAGAGACGAGATCATCAAGGTTATAGATGC 305
QY 61 LysProHisSerGlnProTrpGlnAlaAlaLeuPheGlnLysThrArgLeuLeuGlyCys 80
DB 306 AGGCTCTACTACAGGCATGCGCAGGTGGCCCTCTTTCAGACAGACAGGCTTCTGTGGG 365
QY 81 AlaThrLeuIleAlaProArgTrpLeuLeuThrAlaAlaHisCysLeuLysProArgTyr 100
DB 366 GCAACCTCATGCGCCCAATGGCTCTGACAGCAGCCACTGCGCGCAAGCCCATTAAC 425
QY 101 IleValHisLeuGlyGlnHisAsnLeuGlnLysGlyGlnLysGlnThrArgThr 120
DB 426 GGATCTCTCTGGAGGACCAATCTAGAGAAAGACAGAGCGCTGTAGCAGAGCGGATG 485
QY 121 AlaThrGlnLysPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
DB 486 GGCACCTGATCTCTCCCAACCCCACTTCAACACAGGCTCCCAACAAACACACCGG 545
QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
DB 546 AATGACATATGCTCTGTGAAGATGCTCTCCGCTCTTTACCCGAGCTGTGACAGCA 605
QY 161 LeuThrLysSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
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QY 221 AlaSerValGlnGlnLysGlyLysAspSerCysGlnIleAspSerGlyGlyProLeuVal 240
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QY 261 LysProGlyValIleThrLysValCysLysTyrValAspTrpIleGlnGluThrMetLys 280
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QY 281 AsnAsn 282
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DB 966 AACAAAT 971

RESULT 6
 AK009720
 LOCUS
 DEFINITION

1295 bp mRNA linear HTC 05-DEC-2002
 Mus musculus adult male tongue cDNA. RIKEN full-length enriched library, clone:2310040f07 product:protease, serine, 20, full insert sequence.
 AK009720
 AK009720.1 GI:12844688
 VERSION
 KEYWORDS
 HTC; CAP trapper.
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS

1
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)

2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)

3
 Shibata, K., Itoh, M., Aizawa, K., Nagoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, U., Nishi, K., Kitsumi, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kaishiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Iwawa, M., Ohara, E., Matsumi, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuzaki, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)

4
 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aikawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S., Aikawa, K., Iwawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamataka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, M., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Tomita, M., Quackenbush, J., Schiml, L.M., Stebbins, F., Suzuki, K., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsi, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzatelli, D., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schombach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyokawa, K., Wang, K.H., Weitz, C., Willeker, C., Wilming, L., Wyshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohetsuki, S. and Hayashizaki, Y.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409 (6821), 685-690 (2001)

5
 The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)

6
 (bases 1 to 1295)

REFERENCE	Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
AUTHORS	Carninci, P. and Hayashizaki, Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
MEDLINE	99279253
PUBMED	10349636
REFERENCE	2
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE	11042159
PUBMED	20499374
REFERENCE	3
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsuna, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasaiwa, K., Yonidake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE	RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE	20530913
PUBMED	11076861
REFERENCE	4
AUTHORS	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aikawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yananaka, I., Saito, F., Okazaki, Y., Ashburner, M., Batalov, S., Casavant, T., Kadota, K., Matsuda, H., Asbunier, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kushl, P., Lewis, S., Matsuo, Y., Nikola, I., Pesole, G., Quackenbush, J., Schriml, L.M., Stabli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombert, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyokawa, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L., Wyshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, H., Kohsaki, S. and Hayashizaki, Y.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409 (6821), 685-690 (2001)
MEDLINE	21085660
PUBMED	11217851
REFERENCE	5
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
MEDLINE	12117851
PUBMED	12117851
REFERENCE	6
AUTHORS	Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanaagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Koda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Yamatsu, M. and Hayashizaki, Y.
TITLE	Direct Submission
JOURNAL	Submitted (10-JUL-2000) Yoshinide Hayashizaki, The Institute of

COMMENT	Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-72 Suenhiro-cho, Tsurumi-ku, Yokohama Kanagawa 220-0045, Japan (E-mail: genome-res@gs.c.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216) Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.				
FEATURES	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGCAGAGAGAGATCCACAGAGCTCTTTTATTTTATTTTNN 3'], cDNA was prepared by using trihalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGCAGAGAGATTCGAGTTATTAATTAATATCCCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI, 3' end: SstI. Host: SOLR.				
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	/db_xref="MGI:1894042"				
	/db_xref="taxon:10090"				
	/clone="2310037E23"				
	/sex="male"				
	/tissue_type="longue"				
	/clone_lib="RIKEN full-length enriched mouse cDNA library"				
	/dev_stage="adult"				
	119..948				
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	/db_xref="MGI:1929977"				
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	/note="putative"				
polyA_site	1269				
	/note="putative"				
BASE COUNT	307 a 363 c 304 g 295 t				
ORIGIN					
Alignment Scores:					
Pred. No.:	5..51e-97	Length:	1269		
Score:	1161.00	Matches:	216		
Percent Similarity:	86.88%	Conservative:	29		
Best Local Similarity:	76.60%	Mismatches:	31		
Query Match:	76.23%	Indels:	7		
DB:	11	Gaps:	2		
US-09-856-320A-2 (1-282) x AK009659 (1-1269)					
QY	1	MeGlnArgLeuAlaGtrIleuAlaArgAspIrrPlySerSerGlyArgGlyLeuThAlaAla	20		
Db	119	ATAGAGAGGCTGAAG-----AGTACGAGGAATATCT-----ACAGAAACC	160		
QY	21	LysGluProGlyValAlaGserSerProLeuGlnAlaMetArgIleLeuGlnIleLeu	40		
Db	161	AGGAAACCTGGGCGCCGCTGCTCCCTACTCCAGGCCAGAGATTCCTCCAGTATTGCA	220		
QY	41	IleuAlaIleuAlaThrGlyLeuValGlyGlyIleuThrArgIleIleuGlyPheGluCys	60		
Db	221	CTTGCTCTGTAAACAGGGACGCTAGGGGAGAGACAGATCATCAAGGCTTATGAGTGC	280		
QY	61	LysProHisSerGlnProTrrGlnAlaIleuPheGluIlysthrArgLeuLeuCysGly	80		
Db	281	AGGCTTCATCTCAGCCATGCGAGGTGGCCCTTTTCAAGAGACAGGCTTCTTGGG	340		
QY	81	AlaThrIleuAlaAlaProArgTrrPheuLeuThrAlaAlaHisCysLeuLysProArgTyr	100		
Db	341	GCAACCTATGCCCCCAATAGTCTCTTGACAGACAGCCCATCTCCGCAAGCCCCATTAC	400		


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QY 101 lleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlnGlyCysGluGlnThrArgThr 120
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Db 401 GTGATCTCTCTTGAGAGGACAACTTAGAGAAACAGACGGCTGTAGCGAGG-CCGAG 459
QY 121 AlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArg 140
    ::::::::::::::::::::
Db 460 GGCACGTAGCTCTTCCCGCCCGACTTCMAACAGAGCTCCCGCAACAAAGCACCGG 519
QY 141 AsnAspIleMetLeuValLysMetAlaSerProValSerIleThrTrpAlaValArgPro 160
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Db 520 AATGACATATATGTTGTAAGATGTGCTCCGCTCTTTTACCGGAGCTGTGAGCCCA 579
QY 161 LeuThrLysSerSerArgCysValThrAlaGlyThrSerCysLeuIleSerGlyTrpGly 180
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Db 580 CTCACCTGTCCCGACACTGTCTGCTGACGAGCACACAGCTGCTTCTTGATGGGG 639
QY 181 SerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIleThrIle 200
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Db 640 ACCACGCTCCAGCCCGCAGTTGGCGCTGCTCATTCCTTGATGTGCAATGTCTCCAT 699
QY 201 lleGluHisGlnLysCysGlnAsnAlaTyrProGlyAsnIleThrAspThrMetValCys 220
    ::::::::::::::::::::
Db 700 ATCGAACAACAGAGAGTGTGAAGAGGCTTACCGGACACATCACAGACACATGCTGTG 759
QY 221 AlaSerValGlnGlnGlyLysAspSerCysGlnGlyAspSerGlyLysProLeuVal 240
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Db 760 GCCAGTGTTCGGAAGAGGCAAGAGACTCTGTGACAGGTGACTGTGAGAGCCCCCTGAT 819
QY 241 CysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIleThrArg 260
    ::::::::::::::::::::
Db 820 TCCACACGAGTCTTCTTCAAGGCATCATCTCTGGGGTCAAGACCATGTGCTCCGACACA 879
QY 261 LysProGlyValTyrThrLysValCysLysTyrValAspTrpIleGlnGlnThrMetLys 280
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Db 880 AAGCCGTGGTCTATACAAAGCTGCATAATACTTTAACTGATTCACAGAGTTATAGAG 939
QY 281 AsnAsn 282
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Db 940 AACAAAT 945

RESULT 8
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LOCUS 603037514F1 NIH_MGC_115 Homo sapiens CDNA clone IMAGE:5178746 5'
DEFINITION
    mRNA sequence.
ACCESSION BI818697
VERSION BI818697
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 841)
NIH-MGC http://mgs.nci.nih.gov/.
Mammalian Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHM11445 row: k column: 03
High quality sequence stop: 784.
Location/Qualifiers
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FEATURES
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source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH MGC Library."

BASE COUNT      180 a      288 c      206 g      167 t

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Alignment Scores:
Pred. No.:      5,63e-97      Length:      841
Score:          1158.00      Matches:      222
Percent Similarity: 97.38%      Conservative: 1
Best Local Similarity: 96.94%      Mismatches: 1
Query Match:    76.03%      Indels:      5
DB:              12          Gaps:        0

US-09-856-320A-2 (1-282) x BI818697 (1-841)

QY 59 GluCysLysProHisSerGln-ProTrpGlnAlaLeuPheGluLysThrArgLeu 78
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Db 2 GAGTCAAGCCTCATCTCCAGTCCCTGTGAGGACACCCGTTCGAGAAACCCGGTACT 61
QY 78 uCysGlnAlaThrLeuIleAlaProArgTrpLeuThrAlaAlaHisCysLeuLysPr 98
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Db 62 CTGTGGGGGAGAGCTCATATCGCCCGAGATGCTCTTGACAGACGCCATGCTCAAGCC 121
QY 98 oArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlnGlyCysGluGln 118
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Db 122 CCGTACATAGTTCACTGGGGGACACAACTCCAGAAAGAGAGGGCTGTGAGAGACAG 181
QY 118 rArg-ThrAlaThrGluSerPheProHisProGlyPheAsnAsnSerLeuProAsnLys 138
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Db 182 CTTGACAGCCCACTAGTCTTCCCGCCACCCCGGTTCAACAAAGCCTCCCAACAAAG 241
QY 138 sPheArgAsnAspIleMetLeuValLysMetAlaSerProValSer-IleThrTrpAla 157
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Db 242 ACCACCGCATATACATCTGCTGTGAAGATGGATCCGCACTCTCTATACCTGGGCT 301
QY 158 ValArgProLeuThrLysSerSerArgCysValThrAlaGlyThrSerCysLeuIleSer 177
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Db 302 GTGCGACCCCTACCTCTCTCCACGCTGTGCATGCTGGGACAGCAGCTGCTCATTTCC 361
QY 178 GlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsn 197
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Db 362 GGCTGGGGGACAGACCTCCAGCCCGCAGTTAGCCCTGCTCACCTTGGAAGGCCCAAC 421
QY 198 lleThrIleIleGluHisGlnLysCysGlnAsnAlaTyrProGlyAsnIleThrAspThr 217
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Db 422 ATACCATCATTTAGACACCAAGATGTAGAACGCTTACCCCGGCAACATTCACAGACAC 481
QY 218 MetValCysAlaSerValGlnGln-GlyGlyLysAspSerCysGlnGlyAspSerGlyG 237
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Db 482 ATGGGTGTGTCAGAGGTGACAGAGAGGGGCAAGAGCTCTGCGAGGGTATCCGGGGG 541
QY 237 rProLeuValCysAsnGlnSerLeuGln-GlyIleIleSerTrpGlyGlnAspProCys 257
    ::::::::::::::::::::
Db 542 CCCTTGCTGTGTAACCAAGTCTTTCAATGCAATATATCTCTGGGGGCAAGATTCGTTG 601
QY 257 laIleThrArgLysProGlyValTyrThrLysValCysLysTyrValAspTrpIleGln 277
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Db 602 CGATCACCCGGAAGCGTGTGTCTACAGAAAGTGTCAATATATGTGACTGATTCAGG 661
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Alignment Scores:

Pred. No.: 1,21e-92 Length: 708
 Score: 1110.00 Matches: 208
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 72.88% Indels: 0
 DB: 10 Gaps: 0

US-09-856-320a-2 (1-282) x BG697071 (1-708)

QY 22 G1uPrgGlyAlaArgSerSerProLeuGlnAlaMetArgLLeuGlnLeuLeu 41
 DB 82 GAACCTGGGGCCCGCTCTCCCTCCAGGCGCATGAGATCTGCAGTTAATCTGCTT 141
 QY 42 AlAlaLeuAlaThrgLysLeuValGlyGlyGlyThrArgLLeuLysGlyPheGlyCysLys 61
 DB 142 GCTCTGGACACAGGGCTTGTAGGGGAGACACAGATCATCAAGGGGTTGAGTCAAG 201
 QY 62 ProH1SerGlnProTrrpGlnAlaAlaLeuPheGlyLysThrArgLeuLeuCysGlyAla 81
 DB 202 CCTCACTCCAGCCCTGGCAGGAGCCCTTGTGAGAAGAAGCGGCTACTGTGGGGCG 261
 QY 82 ThrLeuLLeuAlaProArgTrpLeuLeuThraAlaAlaHisCysLeuLysProArgTrp 101
 DB 262 ACAGCTCATGCGCCCGAGATGGCTCTGACAGACAGCCACCTGCTCAAGCCCGCTACATA 321
 QY 102 ValHisLeuGlyGlnHisLeuGlnLysGlyGlyGlyCysGlyGlnThrArgThraAla 121
 DB 322 GTTCACCTGGGAGACACACCTCCAGAAAGAGAGGGCTGTGAGACAGACCCGACAGCC 381
 QY 122 ThrGlySerPheProHisProGlyPheAsnAsnSerLeuProAsnLysAspHisArgAsn 141
 DB 382 ACTGAGTCTCTCCCAACCCCGCTTCAACACAGCTCCCAACAAAGACACCGCAAT 441
 QY 142 AspLLeuLeuValLysMetAlaSerProValSerLLeuThraAlaValArgProLeu 161
 DB 442 GACATCATCTGGTGAAGATGGCATGGCAGTCTTCATCAGCTGGGCTGTGGAGACCCCTC 501
 QY 162 ThrLeuSerSerArgCysValThraAlaGlyThrSerCysLeuLLeuSerGlyTrpGlySer 181
 DB 502 ACCCTTCTCAGCTGTCTCATGTGTGACACAGCTGCTCATTTCCGGCTGGGGCAGC 561
 QY 182 ThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnLLeuThraLLeu 201
 DB 562 ACCTCAGCCCGCAGTACGCTGCTCAGCTTCCAGTGGCCCAACTCACCATCATTT 621
 QY 202 G1uH1eGlnLysCysGlnAsnAlaTrpProGlyAsnLLeuThraAspThrMetValCysAla 221
 DB 622 GAGACACCAAGAGTGAAGAGCGCTTACCCCGGCAACATCAGACACCATGTGTGTGCC 681
 QY 222 SerValGlnGlnGlyGlyLysAsp 229
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 DEFINITION mRNA sequence.
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 VERSION BE867930.1 GI:10316706
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 973)
 AUTHORS NIH-MGC http://mgi.mgi.nhl.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-r@mail.nih.gov
 Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1AM9562 row: a column: 06
 High quality sequence stop: 714.
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 Average insert size 1.8 kb. Library constructed by Life
 Technologies."

BASE COUNT 241 a 302 c 142 t
 ORIGIN

Alignment Scores:

Pred. No.: 3.37e-84 Length: 973
 Score: 1021.00 Matches: 224
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 Best Local Similarity: 81.75% Mismatches: 32
 Query Match: 67.04% Indels: 11
 DB: 10 Gaps: 4

US-09-856-320a-2 (1-282) x BE867930 (1-973)

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 DB 98 ATGCAGAGGTTAGGTGGCTGGCGGAGTGAAGTATCGGCGAGAGCTTCACAGACGCC 157
 QY 21 LysGlnProGlyAlaArgSerSerProLeuGlnAlaMetArgLLeuGlnLeuLLeu 40
 DB 158 AAGGAACCTGGGGCCCGCTCTCCCGCCAGGCGCATAGGATTCGACAGTTAATCTCG 217
 QY 41 LeuAlaLeuAlaThr-GlyLeuValGlyGly---GluTrArgLLeuLysGlyPheGly 59
 DB 218 CTGCTCTGGCAGCAGGGCTGTGTAGGGGGAAGACACAGATATCATCAAGAGGGGTTCCA 277
 QY 59 UCysLysProHisSerGlnProTrrpGlnAlaAlaLeuPheGlyLysThraArgLeuLys 79
 DB 278 GTGCAAGCTCATCTCCAGCCCTTGGCAGGACGCCCTGTTCAAGAAAGCCGGCTACTCTG 337
 QY 79 G1YAlaThrLeuLLeuAlaProArgTrpLeuLeuThraAlaHisCysLeuLysPro-- 98
 DB 338 TGGGGCGAGCTCATCTCCAGCCCGCAGATGGCTCTGACAGAGCCCACTGCTCAAGCCG 397
 QY 99 --ArgTrLLeuValHisLeuGlyGlnHisAsnLeuGlnLysGlnGlyCysGlnLLeu 118
 DB 398 GCCGCTAATAGTTACCTGGGGGAGACACAACTTCAGAAAGAGGGGCTGTGAGCAGA 457
 QY 118 hrArgThraAlaThrgLysLeuValLysMetAlaSerProValSerLLeuThraLLeu 138
 DB 458 CCGGAGACGACCTAGTCTTCCCAACCCGGCTTCAACACAGAGCTCCCAAGAAAG 517
 QY 138 sPh1ArgAsnAspLLeuLeuValLysMetAlaSerProValSerLLeuThraLLeu 158
 DB 518 ACCACCGCAAGACATCATGTGTGAGAGATGGATCCCACTTCATCAGCTGGGCTG 577
 QY 158 a1ArgProLeuThrLeuSerSerArgCysValThraAlaGlyThrSerCysLeuLLeu 178
 DB 578 TGGGACCTTC-ACCTCTCTCAGCTGTGTACTGTGGACCAAGTGGCTCATTTTCG 636
 QY 178 1YTrp-GlySerThr-SerSerProGlnLeuArgLeuProHisThraLLeuArgCysAla 197
 DB 637 GCTGGGGGACAGACAGTCCAGGCCCACTTACGCTGCTCACACACTTGGAGTGGCCAA 696

QY 197 nllrthrllellgllhllgllnlycsgllasnalatYrProGlyAsnllleThraspTh 217
 Db 697 CATCATCATCATATAGACACCAAGTGGTGAACGCATATCCCGGCAACATACAGACAC 756
 QY 217 rnetalYcS-AlaserValngInglYcLYleAspserCysgInglYAspsergYc 237
 Db 757 CATGGTGTGTCCAGCCTGACGACGAGGGGACCCGATCATGCCAAAGTGAAGCCGGG 816
 QY 237 lYrleuValCysasnInserleuInglYlleSerTrpGlylnaProCysA 257
 Db 817 ACCCATGGGCTGTATCACCAGCCCGC-AAGGA---TAATCCGGGGCCAGACCGGAG 872
 QY 257 lallrThrArglyspProGlyValYrThrLys 267
 Db 873 CG---ACACCGGAAGCTGGAGTTACAAAAAG 901
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 ACCESSION BG747134
 VERSION BG747134.1 GI:14057787
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 639)
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgrabbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: NIH Intramural Sequencing Center
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LCM1710 row: k column: 14
 High quality sequence stop: 638.
 Location/Qualifiers
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 /mol_type="mRNA"
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 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 15"
 /notes="Organ: colon; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; CDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-CDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)"
 BASE COUNT 128 a 241 c 162 g 108 t
 ORIGIN
 Alignment Scores:
 Pzed. No.: 3,24e-80 Length: 639
 Score: 975.00 Matches: 187
 Percent Similarity: 99.478 Conservatave: 1
 Best Local Similarity: 98.948 Mismatches: 1
 Query Match: 64.028 Indels: 1
 DB: 10 Gaps: 0
 US-09-856-320a-2 (1-282) x BG747134 (1-639)

QY 22 GluProGlyAlaArgSerSerProleuGlnAlaMetArgllleleuGlnleu 41
 Db 73 GAACCTGGGGCCCGCTCTCCCTCCCTCCAGCCCATGAGATTCCTGACTTCTGCTT 132
 QY 42 AlaleuAlaThrnglyleuValGlyglunhrprglllellelygllPheGllCysLys 61
 Db 133 GCTTGGGACAGAGGCTTGTMG-GGAGAGACAGATCATCAAGGGGTGAGTGAAG 191
 QY 62 ProHISerGlnProTrpGlnAlaAlaleuPheglunhrsthrArgleuLeuCysAla 81
 Db 192 CCTACTCCAGCCCTGGCAGGAGCCCTGTTCAGAAAGACGGGCTACTCTGTGGGGCG 251
 QY 82 ThrleuIleAlaProArgTrpLeuThralaAlahIScYsleuLysProArgTyrIle 101
 Db 252 ACGCTCATCGCCCGCCAGATGCTCTTGACACAGCCCTCCCAAGCCCGGCTACATA 311
 QY 102 ValHISleuGlyglHISAsnleuGlnlysgInglYcYsgInglYnThrArgThraAla 121
 Db 312 GTTACCTGGGGGACAGACACCTCCAGAGAGAGGGCTGTGACAGACCCGGACAGCC 371
 QY 122 ThrGluSerPheProHISProGlyPheAsnAsnSerleuProAsnLysaspHISArgasn 141
 Db 372 ACTGAGTCTTCCCCACCCCGGCTTCAACAACAGCTCCCAACAAGACACCGCAT 431
 QY 142 AspIleMetleuValLysMetAlaSerProValSerIleThrTPAlaValArgProleu 161
 Db 432 GACATCATGCTGGTGAAGATGGATCGGCACTTCATCAGCTGGGCTGTGACCCCTC 491
 QY 162 ThrleuSerSerArgCysValThralaGlyThrSerCysleuIleSerGlyTyrGlySer 181
 Db 492 ACCCTCTCTCAAGCTGTGTCTGCTGCGACCAAGCTGCTCATTTCCGGCTGGGGAC 551
 QY 182 ThrSerSerProGlnleuArgleuProHISThrleuArgCysAlaAsnIleThrIle 201
 Db 552 ACGTCACACCCCAAGTATCGCTGCTGCATCAGCTTGCATGCGCAACATCATCAT 611
 QY 202 GluHISGlnLysCysGluAsnAlaTyr 210
 Db 612 GAGCACCAAGATGTGAAGACGCTTAC 638
 RESULT 13
 BM837078 539 bp mRNA linear EST 06-MAR-2002
 LOCUS BM837078
 DEFINITION K-EST0113029 S9SNU601 Homo sapiens CDNA clone S9SNU601-64-B01 5',
 mRNA sequence.
 ACCESSION BM837078
 VERSION BM837078.1 GI:19193487
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 539)
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished
 COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52, Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.krdb.re.kr
 Plate: 64 row: B column: 01
 High quality sequence stop: 539.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"

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/clone="S9SNU601-64-B01"
/sex="M"
/tissue_type="Ascites"
/cell_type="Epithelial"
/cell_line="SNU-601"
/lab_host="Top10F"
/clone_lib="S9SNU601"
/notes="Organ: Stomach; Vector: pME18-FU3; Site 1: XhoI;
Site 2: XhoI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then deacapped
with tabacco acid pyrophosphatase (TAP). The deacapped
intact mRNA was ligated with DNA-RNA linker including SfiI
site by treatment of 14 RNA ligase and the first strand
cDNA was synthesized with Superscript II using SfiI
oligo-dt primer. After first strand synthesis, RNA was
degraded by NaOH treatment and cDNA was amplified by PCR
reaction. The PCR products were digested with SfiI and
cloned into DraIII-digested pME18-FU3 vector. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

```

```

BASE COUNT      106 a      204 c      139 g      90 t
ORIGIN

```

Alignment Scores:

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Pred. No.:      1 31e-65      Length:      539
Score:          816.00      Matches:      154
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    53.58%      Indels:      0
Db:             12          Gaps:      0

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```

US-09-856-320A-2 (1-282) x BM637078 (1-539)

```

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QY      22 GIUPTGGLAALARGSERPEROLEUGINALAMETARGILEUENLEULEU 41
Db      77 GAACCTGGGGCCGGCTCTCCCTCCAGGCATAGAGATTCTGAGTTAATCCGCTT 136
QY      42 AALALEALATHGILYUENVALGILYUENRARGILELLELYSGILYUENGLYS 61
Db      137 GCTCTGGCAACAGGGCTTGTAGGGGAGAGACAGCATCATCAGGGGTTCCAGTCCAA 196
QY      62 PROHISSEGLINPROTRGGINALALEUPHEGLULYVTHARGLEUENUCYSGILY 81
Db      197 CCTCACTCCAGCCCTGGAGGAGGAGCCCTGTTGAGAGACGGGGGCTACTGTGGGGCG 256
QY      82 THLEULLEALPROARGTRPLEUENUTRALAALAHICYSLEULYSPROARGTYRILE 101
Db      257 AGGCTCATGGCCCCCGAGATGGCTCCGACAGACAGCCCACTGCTCAAGCCCGCTACATA 316
QY      102 VALHISLEUGILYLNHISANLEUGILYUENGLYUENGLYUENGLYUENGLYUEN 121
Db      317 GTTCACTCTGGGAGAGCAACCTCCGAGAGGAGGCTGTAGAGACCCGGACAGCC 376
QY      122 THNGUSERPHEPROHISPROGLYPHESANANSENSELEUPROASNLYSAPHISARGAN 141
Db      377 ACTGAGCTCTTCCCAACCCCGCTTCAACAACAGGCTCCCAACAAGACACACCGCAT 436
QY      142 ASPILEMETLEUVALYUENMETALASERPROVALISERILETHTRPALAVAILARGPROLEU 161
Db      437 GACATCATCTGCTGTAAGATGCGCATGCGCATGCTCATCATCACTGGGCTGTGGACCCCTC 496
QY      162 THLEUSERSERARGCYVALTHRALAGILYTHSERCYSELEU 175
Db      497 ACCCTCTCTCCTCAGCGTGTGTCACTGCTGCGACACAGCTGCCTC 538

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RESULT 14
LOCUS      B1046611      579 bp      mRNA      linear      EST 14-JUN-2001
DEFINITION MR3-FN0206-070201-013-e10 FN0206 Homo sapiens cDNA, mRNA sequence.
ACCESSION  B1046611
VERSION    B1046611.1 GI:14453233

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```

KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 579)
Dias Neto, E., Garcia Correa, R., Varjowski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., von Gienel, C.V., O'Hare
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202653
JOURNAL      MEDLINE
PUBMED      10737800
COMMENT      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=MR3&t2=MR3-FN0206-
070201-013-e10&t3=2001-02-07&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 393.

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FEATURES

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source

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1..579
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="FN0206"
/notes="Organ: prostate normal; Vector: puc18; Site_1: SmaI
; Site_2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
Application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the puc 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."

```

```

BASE COUNT      121 a      180 c      172 g      106 t
ORIGIN

```

Alignment Scores:

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Pred. No.:      1.59e-63      Length:      579
Score:          794.00      Matches:      164
Percent Similarity: 89.36%      Conservative: 4
Best Local Similarity: 87.23%      Mismatches: 16
Query Match:    52.13%      Indels:      6
Db:             12          Gaps:      1

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US-09-856-320A-2 (1-282) x B1046611 (1-579)

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QY      1 METGINARGLEUARGTRPLEUARGSPTRPYSSERSEGLYARGILYUENUTRALA 20
Db      16 TTGCAGAGATTGAGTGTGCTCGGAGCATGGAAGTATCGGACAGAGTCTCACACAGCC 75
QY      21 LYSGLUPROGLYALARGSERSEPEROLEUGINALAMETARGILEUENLEULEU 40
Db      76 AAGGAACCTGGGGCCGGCTCTCCCTCCAGGCGCATAGAGATTCTCAGTTAATCCTG 135
QY      41 LEUALALEALATHGILYUENVALGILYUENRARGILELLELYSGILYUENGLYUEN 60
Db      136 CTTCCTCTGTCAACAGGCTTGTAGGGGAGAGACAGCATCATCAAGGGTTCAGATGC 195
QY      61 LYSPROHISSEGLINPROTRGGINALALEUPHEGLULYVTHARGLEUENUCYSGILY 80
Db      196 AAGCTCACTCCAGCCCTGGAGGACAGGCTGTTGAGGAAGATGCGGCTACTGTGG 255

```

```

QY      81 AAThtleuileAaProArtrtpleuLeuThraAaHicCysleuLysProArgrTyr 100
Db      256 GGGAGGCTATGCCCCCGAGATGGCTCCGAGACAGACCCACTGCTCAAGCCCCGCTAC 315
QY      101 ILeValHisLeuGlyGlnHisAsnLeuGlnLysGlnGlyCysGlnGlnThrArgTrpThr 120
Db      316 AATGTTCACTGGGGGAGACACAACTCCGAAAGAGAGAGGCTGTGAGCAGACCCGAGACA 375
QY      121 AATArgLysSerPheProHisProGlyPheAsnAsnSerLeu-ProAsnLysAspHisArg 140
Db      376 GCCACTGAGTCTCTCCCCCAGCCGGGATTCAACAGAGGCTCCCCAAAAAGACCACTG 435
QY      140 GAsnAspLysMetLeuValLysMetAlaSerProVal-SerIleThr-TryAlaValArg 159
Db      436 CAATGACATCATGCTGTGTGAAGATGCGCATGCGCAGTCTTCATCACTTGCGCTGGGGA 495
QY      160 ProLeuThrLysSerSerArgCysValThrAlaGlyThrSerCysLeuLysSerGlyTrp 179
Db      496 CCCCTCAA-CTCTCTCAAGCTGTGT-ACTGCTGGCCAGCTGCTCATTTTC--GGCTGG 550
QY      180 GlySerThrSerSerPro 185
Db      551 GGGCAGAGCTCAGCCCA 568

RESULT 15
LOCUS   BM982377.1 761 bp mRNA linear EST 21-FEB-2003
DEFINITION UI-CF-EN1-acs-o-17-0-UI-s1 UI-CF-EN1 Homo sapiens CDNA clone
          BM982377
KEYWORDS  EST.
ACCESSION BM982377.1 GI:19605813
VERSION   1
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 761)
          Bonaldo,M.F., Lennon,G. and Soares,M.B.
          Normalization and subtraction: two approaches to facilitate gene
          discovery
          Genome Res. 6 (9), 791-806 (1996)
JOURNAL   97044477
MEDLINE   8889548
PUBMED    97044477
COMMENT   Contact: McCray, PB
          McCray Lab
          University of Iowa
          2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
          Tel: 319 356 4866
          Fax: 319 356 7171
          Email: paul-mccray@uiowa.edu
          Tissue Procurement: Dr. M. J. Welsh, University of Iowa
          CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
          CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
          DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
          Genetics (www.researchgen.com) or from Open Biosystems
          (www.openbiosystems.com).
          The following repetitive elements were found in this CDNA
          sequence: 17-100, >LINE2 (matched complement)
          Seq primer: M13 FORWARD
          POLYA=Yes.

FEATURES
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         /organism="Homo sapiens"
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         /db_xref="taxon:9606"
         /clone="UI-CF-EN1-acs-o-17-0-UI"
         /tissue_type="Primary Lung Cystic Fibrosis Epithelial
         Cells"
         /dev_stage="Adult"
         /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
         /clone_id="UI-CF-EN1"

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```

/note="Organ: Lung; Vector: pRTT3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I.
UI-CF-EN1 is a normalized CDNA library containing the
following tissue(s): Primary Lung Cystic Fibrosis
Epithelial Cells. The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was ligated to an EcoR I adaptor, digested with Not
I, and cloned directionally into pRTT3-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (d)18 tail. The
sequence tag for this library is CTGCTCAGGT.
TAG_Lib=UI-CF-EN1
TAG_Tissue=Human Lung Epithelial Cell Lines untreated LPS
6hr to LPS 24h
TAG_SEQ=CTGCTCAGGT"

BASE COUNT      172 a      170 c      222 g      195 t      2 others
ORIGIN

Alignment Scores:
Pred. No.:      4,73e-62      Length:      761
Score:          780.00      Matches:      143
Percent Similarity: 99.31%      Conservative: 0
Best Local Similarity: 99.31%      Mismatches: 1
Query Match:      51.21%      Indels: 0
DB:              12      Gaps: 0

US-09-856-320a-2 (1-282) x BM982377 (1-761)
QY      139 HisArgAsnAspLysMetLeuValLysMetAlaSerProValSerIleThrTryAlaVal 158
Db      761 CACCGCAATGACATCATGCTGTGGAAGATGSCATCGCAGTCTCATCATCCTGGAGCTGTG 702
QY      159 ArgProLeuThrLysSerSerArgCysValThrAlaGlyThrSerCysLeuLysSerGly 178
Db      701 CGACCCCTCACCTCTCTCTCAAGNTGTCTACTGTGGACACCACTGCTCATTTCCGCG 642
QY      179 TrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeuArgCysAlaAsnIle 198
Db      641 TGGGACAGACAGTCACAGCCCGGAGTTAGCCTGCTCACACCTTGCGATGGCCAACTC 582
QY      199 ThrIleIleGlnHisGlnLysCysGlnAsnAlaTyrProGlyAsnIleThrAspThrMet 218
Db      581 ACCATCATTTGACACCAAGAGTGAAGAACCCCTAACCCCGCAATCAGACACCATG 522
QY      219 ValCysAlaSerValGlnGlnGlyGlyLysAspSerCysGlnGlyAspSerGlyPro 238
Db      521 GTGTGTGCCAGCTGCGAGAAAGGGGCAAGGACTCTGCGAGGTACTCCGGGGGCTT 462
QY      239 LeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGlnAspProCysAlaIle 258
Db      461 CTGCTGTATACAGTCTCTTCAAGGATTAATCTCTGGGGCCAGATTCGTTGGCATC 402
QY      259 ThrArgLysProGlyValTyrThrLysValCysLysTyrValAspTrpIleGlnGluThr 278
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QY      279 MetLysAsnAsn 282
Db      341 ATGAAGAAACAT 330

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Search completed: October 23, 2003, 19:18:40
Job time : 2437.21 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 22, 2003, 15:46:12 ; Search time 34.0587 Seconds
(without alignments)
1067.227 Million cell updates/sec

Title: US-09-856-320a-2_COPY_54_282

Perfect score: 1258

Sequence: 1 IIKGFCECKHSPQWQALFE.....GYTVKVKYDWIIGETMKNN 229

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1258	100.0	250	21	AAAB21325
2	1258	100.0	250	21	AAAY9390
3	1258	100.0	250	22	ABB50479
4	1258	100.0	250	22	AAU12424
5	1258	100.0	250	22	AAAB6139
6	1258	100.0	250	23	ABG61816
7	1258	100.0	250	23	ABR95526
8	1258	100.0	250	23	ABBB4920
9	1258	100.0	250	23	AAU83684

10	1258	100.0	250	24	ABU66822
11	1258	100.0	250	24	ABU67098
12	1258	100.0	250	24	ABU59903
13	1258	100.0	250	24	ABU56739
14	1258	100.0	282	20	AAV42439
15	1258	100.0	282	21	AAAB1712
16	1258	100.0	282	21	AAV43636
17	1252	99.5	281	20	AAV42440
18	1235.5	98.2	275	21	AAAB1714
19	1231	97.9	228	21	AAAB21312
20	1228	97.6	250	20	AAV36093
21	1227	97.5	248	22	AAE08017
22	1219.5	96.9	289	21	AAAB6483
23	1219.5	96.9	289	22	AAAB7543
24	1062	84.4	276	21	AAAB1713
25	1014.5	80.6	247	23	ABG70276
26	736	58.5	250	21	AAAB21298
27	736	58.5	250	23	ABP64969
28	736	58.5	251	22	AAU16971
29	734	58.3	247	22	AAU23217
30	731.5	58.1	296	21	AAAB21297
31	716	56.9	247	22	AAU86677
32	716	56.9	247	22	AAU23752
33	716	56.9	247	22	AAU17043
34	688	54.7	275	21	AAAB21311
35	684	54.4	260	17	AAW10694
36	684	54.4	260	18	AAW12393
37	684	54.4	260	23	ABR57219
38	682	54.2	256	23	AAU79390
39	682	54.2	320	23	AAE19166
40	682	54.2	320	23	AAU82732
41	681	54.1	260	20	AAV41744
42	681	54.1	260	20	AAV32852
43	681	54.1	260	20	AAV03220
44	681	54.1	260	20	AAW87703
45	681	54.1	260	21	AAAB21322

ALIGNMENTS

RESULT 1	
AAAB21325	strand: protein; 250 AA.
AC	AAAB21325;
DT	02-FEB-2001 (first entry)
DE	Human TLP.
KW	Human; KTK-L1; KTK-L2; KTK-L3; KTK-L4; KTK-L5; KTK-L6; TLP;
KW	lysyl-like serine protease; kallikrein-like protein; serine protease;
KW	cytostatic; cancer; prostate cancer.
OS	Homo sapiens.
PN	WO200053776-A2.
PD	14-SEP-2000.
PF	09-MAR-2000; 2000WO-CA00258.
PR	11-MAR-1999; 99US-0124260.
PR	01-APR-1999; 99US-0127386.
PR	21-JUL-1999; 99US-0144919.
PA	(MOUNT) MOUNT SINAI HOSPITAL.
PI	Yousef GM, Diamandis EP;
DR	WPI; 2000-587440/55.

PT New kallikrein-like (KLK-L) proteins for diagnosing and treating KLK-L
PT protein mediated disorders, especially cancer.
XX
PS Example 5; Fig 27; 184pp; English.
XX
CC The present sequence is human trypsin-like serine protease (TLSP), a
CC member of the serine protease family. Kallikreins and
CC kallikrein-like proteins are a subgroup of the serine protease enzyme
CC family. They catalyze the selective cleavage of specific polypeptide
CC precursors to release peptides with potent biological activity. Nucleic
CC acids encoding kallikrein-like proteins KLK-L1, KLK-L2, KLK-L3, KLK-L4,
CC KLK-L5 and KLK-L6 have been isolated. The proteins are useful in the
CC treatment, monitoring and diagnosis of cancers, especially prostate
CC cancer. They can also be used to identify a substance that can associate
CC with or mediate the biological activity of the proteins. Antibodies can
CC be used to treat conditions mediated by the kallikrein-like proteins.
XX
SQ Sequence 250 AA:

Query Match 100.0%; Score 1258; DB 21; Length 250;
Best Local Similarity 100.0%; Pred. No. 6.3e-113;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IIKGFECRPHSQPMQAALEKTRRLCGATLTPRWLTAAHCKRPRIYVHGOHLOKEE 60
Db 22 IIKGFECRPHSQPMQAALEKTRRLCGATLTPRWLTAAHCKRPRIYVHGOHLOKEE 81
OY 61 GGEQRTATESPPHGFNNSLPNKDRNDIMLVKASPVSIWAVRPLTSSRCVTAGTS 120
Db 82 GGEQRTATESPPHGFNNSLPNKDRNDIMLVKASPVSIWAVRPLTSSRCVTAGTS 141
OY 121 CLISWGSTSSPOLRLPHTLRCANITITIEHOKCENAVPONTITDWNVCASVQEGKDCSCG 180
Db 142 CLISWGSTSSPOLRLPHTLRCANITITIEHOKCENAVPONTITDWNVCASVQEGKDCSCG 201
OY 181 DSGGLVNCNOSIQIISWGQDCATTRKRGVTKYCKVVDWIQETMKNN 229
Db 202 DSGGLVNCNOSIQIISWGQDCATTRKRGVTKYCKVVDWIQETMKNN 250

RESULT 2
AAV99390
ID AAV99390 standard; Protein; 250 AA.
XX
AC AAV99390;
XX
DT 08-AUG-2000 (first entry)
XX
DE Human PRO1279 (UNO649) amino acid sequence SEQ ID NO:170.
XX
KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
transmembrane; secretion; immunoadhesion; pharmaceutical; screening.
XX
OS Homo sapiens.
XX
PN WO200012708-A2.
XX
PD 09-MAR-2000.
XX
PE 01-SEP-1999; 99WO-US20111.
XX
PR 01-SEP-1998; 98US-0098716.
PR 01-SEP-1998; 98US-0098749.
PR 01-SEP-1998; 98US-0098750.
PR 02-SEP-1998; 98US-0098803.
PR 02-SEP-1998; 98US-0098821.
PR 02-SEP-1998; 98US-0098843.
PR 09-SEP-1998; 98US-0099536.
PR 09-SEP-1998; 98US-0099596.
PR 09-SEP-1998; 98US-0099598.
PR 09-SEP-1998; 98US-0099602.
PR 09-SEP-1998; 98US-0099642.
PR 10-SEP-1998; 98US-0099741.

PR 10-SEP-1998; 98US-0099754.
PR 10-SEP-1998; 98US-0099763.
PR 10-SEP-1998; 98US-0099792.
PR 10-SEP-1998; 98US-0099808.
PR 10-SEP-1998; 98US-0099812.
PR 10-SEP-1998; 98US-0099815.
PR 10-SEP-1998; 98US-0099816.
PR 15-SEP-1998; 98US-0100385.
PR 15-SEP-1998; 98US-0100388.
PR 15-SEP-1998; 98US-0100390.
PR 16-SEP-1998; 98US-0100584.
PR 16-SEP-1998; 98US-0100627.
PR 16-SEP-1998; 98US-0100661.
PR 16-SEP-1998; 98US-0100662.
PR 16-SEP-1998; 98US-0100664.
PR 17-SEP-1998; 98US-0100683.
PR 17-SEP-1998; 98US-0100710.
PR 17-SEP-1998; 98US-0100711.
PR 17-SEP-1998; 98US-0100919.
PR 17-SEP-1998; 98US-0100930.
PR 18-SEP-1998; 98US-0100848.
PR 18-SEP-1998; 98US-0100849.
PR 18-SEP-1998; 98US-0101014.
PR 18-SEP-1998; 98US-0101066.
PR 18-SEP-1998; 98US-0101071.
PR 22-SEP-1998; 98US-0101279.
PR 23-SEP-1998; 98US-0101471.
PR 23-SEP-1998; 98US-0101472.
PR 23-SEP-1998; 98US-0101474.
PR 23-SEP-1998; 98US-0101475.
PR 23-SEP-1998; 98US-0101476.
PR 23-SEP-1998; 98US-0101477.
PR 23-SEP-1998; 98US-0101479.
PR 24-SEP-1998; 98US-0101738.
PR 24-SEP-1998; 98US-0101741.
PR 24-SEP-1998; 98US-0101743.
PR 24-SEP-1998; 98US-0101915.
PR 24-SEP-1998; 98US-0101916.
PR 29-SEP-1998; 98US-0102207.
PR 29-SEP-1998; 98US-0102240.
PR 29-SEP-1998; 98US-0102307.
PR 29-SEP-1998; 98US-0102310.
PR 29-SEP-1998; 98US-0102331.
PR 30-SEP-1998; 98US-0102484.
PR 30-SEP-1998; 98US-0102487.
PR 30-SEP-1998; 98US-0102570.
PR 30-SEP-1998; 98US-0102571.
PR 01-OCT-1998; 98US-0102684.
PR 01-OCT-1998; 98US-0102687.
PR 02-OCT-1998; 98US-0102965.
PR 06-OCT-1998; 98US-0103258.
PR 06-OCT-1998; 98US-0103449.
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PR 07-OCT-1998; 98US-0103315.
PR 07-OCT-1998; 98US-0103328.
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PR 07-OCT-1998; 98US-0103401.
PR 08-OCT-1998; 98US-0103633.
PR 08-OCT-1998; 98US-0103637.
PR 08-OCT-1998; 98US-0103679.
PR 08-OCT-1998; 98US-0103711.
PR 14-OCT-1998; 98US-0104257.
PR 20-OCT-1998; 98US-0104987.
PR 20-OCT-1998; 98US-0105000.
PR 20-OCT-1998; 98US-0105002.
PR 21-OCT-1998; 98US-0105104.
PR 22-OCT-1998; 98US-0105169.
PR 22-OCT-1998; 98US-0105266.
PR 26-OCT-1998; 98US-0105693.
PR 26-OCT-1998; 98US-0105694.
PR 27-OCT-1998; 98US-0105807.


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PR 27-OCT-1998; 98US-0105881.
PR 27-OCT-1998; 98US-0105882.
PR 27-OCT-1998; 98US-0106062.
PR 28-OCT-1998; 98US-0106023.
PR 28-OCT-1998; 98US-0106029.
PR 28-OCT-1998; 98US-0106030.
PR 28-OCT-1998; 98US-0106032.
PR 28-OCT-1998; 98US-0106033.
PR 28-OCT-1998; 98US-0106178.
PR 29-OCT-1998; 98US-0106248.
PR 29-OCT-1998; 98US-0106384.
PR 29-OCT-1998; 98US-0108500.
PR 30-OCT-1998; 98US-0106464.
PR 03-NOV-1998; 98US-0106856.
PR 03-NOV-1998; 98US-0106902.
PR 03-NOV-1998; 98US-0106905.
PR 03-NOV-1998; 98US-0106919.
PR 03-NOV-1998; 98US-0106932.
PR 03-NOV-1998; 98US-0106934.
PR 10-NOV-1998; 98US-0107783.
PR 17-NOV-1998; 98US-0108775.
PR 17-NOV-1998; 98US-0108779.
PR 17-NOV-1998; 98US-0108787.
PR 17-NOV-1998; 98US-0108788.
PR 17-NOV-1998; 98US-0108801.
PR 17-NOV-1998; 98US-0108802.
PR 17-NOV-1998; 98US-0108806.
PR 17-NOV-1998; 98US-0108807.
PR 17-NOV-1998; 98US-0108867.
PR 17-NOV-1998; 98US-0108925.
PR 18-NOV-1998; 98US-0108848.
PR 18-NOV-1998; 98US-0108849.
PR 18-NOV-1998; 98US-0108850.
PR 18-NOV-1998; 98US-0108851.
PR 18-NOV-1998; 98US-0108852.
PR 18-NOV-1998; 98US-0108858.
PR 18-NOV-1998; 98US-0108904.
XX
XX (GENTH ) GENENTECH INC.
XX
XX Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
XX
XX WPI; 2000-237871/20.
XX
XX N-PSDB; AAA37072.
XX
XX New mammalian DNA sequences encoding transmembrane, receptor or
XX secreted PRO polypeptides, useful for screening of potential peptide or
XX small molecule inhibitors of the relevant receptor/ligand interactions
XX
XX Claim 12; Fig 102; 773pp; English.
XX
XX AAA37022 to AAA37144 encode the new isolated human transmembrane,
XX receptor or secreted PRO polypeptides given in AAY9340 to AAY93462. The
XX transmembrane and receptor PRO proteins can be used for screening of
XX potential peptide or small molecule inhibitors of the relevant
XX receptor/ligand interactions. The polypeptides and nucleotide sequences
XX encoding them have various industrial applications, including uses as
XX pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent
XX PCR primers and hybridisation probes used in the isolation of the PRO
XX polypeptides from the present invention.
XX
XX Sequence 250 AA,
XX
XX Query Match 100.0%; Score 1258; DB 21; Length 250;
XX Best Local Similarity 100.0%; Pred.No. 6,3e-113;
XX Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 IIKGFECKRHPQWQALFEKTRLLCGATLTPRWLLTAHCLKRRIYVHLGQNLQKEE 60
XX IIKGFECKRHPQWQALFEKTRLLCGATLTPRWLLTAHCLKRRIYVHLGQNLQKEE 81
XX
XX GGEOTRIATESPPHGFNNSLPNKDRNDIMLVKMAFPSVITWAVRPLTSSRCVTAGTS 120
XX

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DB 82 GGEOTRIATESPPHGFNNSLPNKDRNDIMLVKMAFPSVITWAVRPLTSSRCVTAGTS 141
XX
QY 121 CLISGWSSTSSPOLPLPHTLRCAANTITIEHQECENAYPNIDTIVCASVQGGKDS CGG 180
XX
DB 142 CLISGWSSTSSPOLPLPHTLRCAANTITIEHQECENAYPNIDTIVCASVQGGKDS CGG 201
XX
QY 181 DSGGPLVNCNQSLOGIISWQDPCATTRKRGVYTKCKYVDWIQETMKNN 229
XX DSGGPLVNCNQSLOGIISWQDPCATTRKRGVYTKCKYVDWIQETMKNN 250
DB
XX
XX RESULT 3
XX ABB50479
XX ID ABB50479 standard; Protein; 250 AA.
XX
XX ABB50479;
XX
XX 07-FEB-2002 (first entry)
XX
XX Human secreted protein encoded by gene 179 SEQ ID NO:427.
XX
XX Human; secreted protein; immunomodulatory; antisclerotic; anti-HIV;
XX dermatological; immunosuppressive; anti-inflammatory; immunostimulant;
XX cytosolic; cardiac; vascular; anti-angiogenic; ophthalmological;
XX neuroprotective; nootropic; anticonvulsant; antialzheimers; vulnary;
XX antiparkinsonian; antimicrobial; gene therapy; vaccine; immune disorder;
XX multiple sclerosis; systemic lupus erythematosus; HIV infection; cancer;
XX human immunodeficiency virus; hyperproliferative disorder; wound healing;
XX Gaucher's disease; cardiovascular disease; Schmitz syndrome; chemotaxis;
XX Chaga's cardiomyopathy; coronary arteriosclerosis; angogenic disorder;
XX corneal graft neovascularisation; diabetic retinopathy; regeneration;
XX neurological disorder; Huntington's chorea; Alzheimer's disease;
XX Parkinson's disease; infectious disease.
XX
XX Homo sapiens.
XX
XX WO200162891-A2.
XX
XX 30-AUG-2001.
XX
XX 21-FEB-2001; 2001WO-US05614.
XX
XX 24-FEB-2000; 2000US-184836P.
XX
XX 29-MAR-2000; 2000US-193170P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ni J, Ebner R, Lafleur DM, Moore PA, Olsen HS, Rosen CA;
XX Ruben SM, Soppet DR, Young PE, Shi Y, Florence KA, Wei Y;
XX Florence C, Hu J, Li Y, Kyaw H, Fischer CL, Ferrie AM, Fan P;
XX Feng P, Endress GA, Dillon PU, Carter KC, Brewer LA, Yu G;
XX Zeng Z, Greene JM;
XX
XX WPI; 2001-625724/72.
XX
XX N-PSDB; ABA83372.
XX
XX Nucleic acids encoding 207 human secreted polypeptides, useful for
XX preventing, diagnosing and/or treating, e.g. cancers, Parkinson's
XX disease and diabetic retinopathy -
XX
XX Claim 11; Page 1181-1182; 1533pp; English.
XX
XX ABB50301 to ABB51287 and ABA83194 to ABA83441 represent human secreted
XX proteins (I) and polynucleotide (II) sequences. (I) and (II) have various
XX activities based on the tissues and cells the genes are expressed in.
XX Example of these activities include: immunomodulatory; antisclerotic;
XX dermatological; immunosuppressive; anti-inflammatory; immunostimulant;
XX anti-HIV; cytostatic; cardiac; anti-angiogenic; ophthalmological;
XX neuroprotective; nootropic; anticonvulsant; antialzheimers; vascular;
XX antiparkinsonian; antimicrobial; and vulnary. (I) and (II) can be used
XX in gene therapy and vaccine production. (I) and (II) can be used in the
XX prevention, diagnosis and treatment of immune disorders (e.g. multiple
XX sclerosis, systemic lupus erythematosus and human immunodeficiency virus
XX

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(HIV) infections), hyperproliferative disorders (e.g. cancers and Gaucher's disease), cardiovascular diseases (e.g. Scimitar syndrome, Chaga's cardiomyopathy and coronary arteriosclerosis), angiogenic disorders (e.g. corneal graft neovascularisation and diabetic retinopathy), neurological disorders (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease), infectious diseases and/or for promoting wound healing, regeneration and/or chemotaxis. ABB83185 to ABB83193 and ABB830300 represent sequences used in the exemplification of the present invention.

Sequence 250 AA:

Query Match 100.0%; Score 1258; DB 22; Length 250;
Best Local Similarity 100.0%; Pred. No. 6.3e-113;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFECKPHSQPQOALFEKTRLLCGATLTPRWLLTAHCLKPRYIVHGGNLOKEE 60
DB 22 IIKGFECKPHSQPQOALFEKTRLLCGATLTPRWLLTAHCLKPRYIVHGGNLOKEE 81
QY 61 GCEQTRTATESFPHGPNNSLPNKHNDIMLVKMASPVSIITWAVRPLTSSRCVTAGTS 120
DB 82 GCEQTRTATESFPHGPNNSLPNKHNDIMLVKMASPVSIITWAVRPLTSSRCVTAGTS 141
QY 121 CLISGWSTSSPOLRLPHTLRCAANTITIEHOKCENAVPGNITDTMVCASVOEGKDSGCG 180
DB 142 CLISGWSTSSPOLRLPHTLRCAANTITIEHOKCENAVPGNITDTMVCASVOEGKDSGCG 201
QY 181 DSGGPLVNCNOSLOGIISWGDPCATTRKPGVYTKVCKYVDMIOETMKN 229
DB 202 DSGGPLVNCNOSLOGIISWGDPCATTRKPGVYTKVCKYVDMIOETMKN 250

RESULT 4

AAU12424 standard; Protein; 250 AA.

AAU12424;

24-OCT-2001 (first entry)

Human PRO1279 polypeptide sequence.

Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy.

Homo sapiens.

MO200140466-A2.

07-JUN-2001.

01-DEC-2000; 2000WO-US32678.

01-DEC-1999; 99WO-US28301.
01-DEC-1999; 99WO-US28634.
02-DEC-1999; 99WO-US28551.
02-DEC-1999; 99WO-US28564.
02-DEC-1999; 99WO-US28565.
09-DEC-1999; 99US-0170262.
16-DEC-1999; 99WO-US30095.
20-DEC-1999; 99WO-US30911.
30-DEC-1999; 99WO-US31243.
06-JAN-2000; 2000WO-US00277.
06-JAN-2000; 2000WO-US00376.
11-FEB-2000; 2000WO-US03565.
18-FEB-2000; 2000WO-US04341.
18-FEB-2000; 2000WO-US04342.
22-FEB-2000; 2000WO-US04414.
24-FEB-2000; 2000WO-US04914.

24-FEB-2000; 2000WO-US05004.
01-MAR-2000; 2000WO-US05601.
20-MAR-2000; 2000WO-US07377.
21-MAR-2000; 2000WO-US07532.
30-MAR-2000; 2000WO-US08439.
17-MAY-2000; 2000WO-US13705.
22-MAY-2000; 2000WO-US14042.
30-MAY-2000; 2000WO-US14941.
02-JUN-2000; 2000WO-US15264.
10-NOV-2000; 2000WO-US30873.

(GENTECH) GENENTECH INC.

Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W, Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S, Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z; WPI: 2001-408281/43.
N-PSDB; AAS21496.

Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. lung, breast, prostate, cervical.

Claim 12, Fig 506; 813pp; English.

AAU12172-AAU12446 represent novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polynucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.

Sequence 250 AA:

Query Match 100.0%; Score 1258; DB 22; Length 250;
Best Local Similarity 100.0%; Pred. No. 6.3e-113;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFECKPHSQPQOALFEKTRLLCGATLTPRWLLTAHCLKPRYIVHGGNLOKEE 60
DB 22 IIKGFECKPHSQPQOALFEKTRLLCGATLTPRWLLTAHCLKPRYIVHGGNLOKEE 81
QY 61 GCEQTRTATESFPHGPNNSLPNKHNDIMLVKMASPVSIITWAVRPLTSSRCVTAGTS 120
DB 82 GCEQTRTATESFPHGPNNSLPNKHNDIMLVKMASPVSIITWAVRPLTSSRCVTAGTS 141
QY 121 CLISGWSTSSPOLRLPHTLRCAANTITIEHOKCENAVPGNITDTMVCASVOEGKDSGCG 180
DB 142 CLISGWSTSSPOLRLPHTLRCAANTITIEHOKCENAVPGNITDTMVCASVOEGKDSGCG 201
QY 181 DSGGPLVNCNOSLOGIISWGDPCATTRKPGVYTKVCKYVDMIOETMKN 229
DB 202 DSGGPLVNCNOSLOGIISWGDPCATTRKPGVYTKVCKYVDMIOETMKN 250

RESULT 5

AAB66139

ID AAB6139 standard; protein; 250 AA.
 XX
 AC AAB6139;
 XX
 DT 02-APR-2001 (first entry)
 XX
 DE Protein of the invention #51.
 XX
 KW Secreted; transmembrane; gene therapy.
 XX
 OS Unidentified.
 XX
 PN WO200078961-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 18-FEB-2000; 2000WO-US04342.
 XX
 PR 23-JUN-1999; 99US-0141037.
 PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 01-SEP-1999; 99WO-US20111.
 PR 29-OCT-1999; 99US-0162506.
 PR 30-NOV-1999; 99WO-US28313.
 PR 02-DEC-1999; 99WO-US28551.
 PR 16-DEC-1999; 99WO-US00219.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00376.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Baker KP, Borstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
 PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
 PI Pan J, Paoletti NF, Roy MA, Smith V, Stewart TA, Tumas D;
 PI Watanabe CK, Williams PM, Wood WI;
 XX
 DR WPI; 2001-071395/08.
 XX
 PT Secreted and transmembrane proteins and nucleic acids designated PRO,
 PT useful as hybridization probes, in chromosome and gene mapping and gene
 PT therapy -
 XX
 PS Claim 1; Fig 102; 787bp; English.
 XX
 CC The present invention relates to secreted and transmembrane proteins.
 CC These proteins and the DNA encoding them may be used as hybridization
 CC probes, in chromosome and gene mapping and in the generation of
 CC anti-sense RNA and DNA. They may also be used to generate either
 CC transgenic animals or knockout animals which are in turn useful for
 CC development and screening of therapeutically useful reagents.
 CC The nucleic acids may also be used in gene therapy.
 CC
 XX
 SQ Sequence 250 AA;
 XX
 Query Match 100.0%; Score 1258; DB 22; Length 250;
 Best Local Similarity 100.0%; Pred. No. 6.3e-113;
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGECKRPHSQPWQALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHLGQHNLOKEE 60
 DB 22 IIKGECKRPHSQPWQALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHLGQHNLOKEE 81
 QY 61 GGEQRTATASFPHGCFNNSLVKDKHRNDIMLVKASPVSTIWAYRPLTLSSRCVTAGTS 120
 DB 82 GGEQRTATASFPHGCFNNSLVKDKHRNDIMLVKASPVSTIWAYRPLTLSSRCVTAGTS 141
 QY 121 CLISGSGTSSPOLRLPHTLRCAANTIIHOKCENAYPNITDITWVCASVOGGKDSOCG 180
 DB 142 CLISGSGTSSPOLRLPHTLRCAANTIIHOKCENAYPNITDITWVCASVOGGKDSOCG 201
 QY 181 DSGGPIVNCQSLGGIISWGQDPCATIRKPGVYTKVCKYDWTQETMKN 229
 DB 202 DSGGPIVNCQSLGGIISWGQDPCATIRKPGVYTKVCKYDWTQETMKN 250

RESULT 6
 ID AAB61816 standard; Protein; 250 AA.
 XX
 AC AAB61816;
 XX
 DT 15-AUG-2002 (first entry)
 XX
 DE Prostate cancer-associated protein #17.
 XX
 KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic.
 XX
 OS Mammalia.
 XX
 PN WO200230268-A2.
 XX
 PD 18-APR-2002.
 XX
 PF 12-OCT-2001; 2001WO-US32045.
 XX
 PR 13-OCT-2000; 2000US-0687576.
 PR 08-DEC-2000; 2000US-0733288.
 PR 08-DEC-2000; 2000US-0733742.
 PR 24-JAN-2001; 2001US-263957P.
 PR 16-MAR-2001; 2001US-276791P.
 PR 16-MAR-2001; 2001US-276888P.
 PR 06-APR-2001; 2001US-281922P.
 PR 24-APR-2001; 2001US-286214P.
 PR 30-APR-2001; 2001US-0847046.
 PR 04-MAY-2001; 2001US-288589P.
 XX
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 XX
 PI Gish KC, Mack DH, Wilson KE, Afar D, Hevez P;
 XX
 DR WPI; 2002-471335/50.
 DR N-PSDB; ABK92131.
 XX
 PT Detecting a prostate cancer-associated transcript in a cell in a
 PT patient, useful for diagnosing prostate cancer (PC) or screening
 PT modulators of PC, by determining if prostate cancer-associated genes
 PT are expressed in a prostate tissue -
 XX
 PS Claim 27; Page 314; 436bp; English.
 XX
 CC The present invention relates to methods of detecting a prostate
 CC cancer-associated transcript in a cell from a patient. The method
 CC comprises contacting a biological sample from the patient with
 CC prostate cancer-associated polynucleotides (designated PC genes) that
 CC selectively hybridize to a sequence that is at least 80% identical
 CC to them. The prostate cancer-associated polynucleotide sequences
 CC are differentially expressed in prostate tumour tissue or in
 CC prostate cancer and are derived from the tissues of various
 CC organisms such as humans or other mammals (e.g. mice, sheep and dogs).
 CC The methods of the invention are useful for diagnosing and treating
 CC prostate cancer in mammals. The prostate cancer-associated genes are
 CC useful for diagnosing or treating prostate cancer, as well as for
 CC identifying modulators of prostate cancer or agents that inhibit
 CC prostate cancer. The nucleic acid sequences are particularly useful
 CC in gene therapy, as a vaccine or in antisense applications.
 CC
 XX
 SQ Sequence 250 AA;
 XX
 Query Match 100.0%; Score 1258; DB 23; Length 250;
 Best Local Similarity 100.0%; Pred. No. 6.3e-113;
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGECKRPHSQPWQALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHLGQHNLOKEE 60
 DB 22 IIKGECKRPHSQPWQALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHLGQHNLOKEE 81

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QY 61 GCEQRTITATSEFPHPGFNNSLPNKDHNDIMLVKMASPVSTITWAVRPLTSSRCVTAGTS 120
DB 82 GCEQRTITATSEFPHPGFNNSLPNKDHNDIMLVKMASPVSTITWAVRPLTSSRCVTAGTS 141
QY 121 CLISGWSGTSPPQLRPLHTLRCAANTITIEHOKCENAYPGNITDTMVCASVOEGGKDSOG 180
DB 142 CLISGWSGTSPPQLRPLHTLRCAANTITIEHOKCENAYPGNITDTMVCASVOEGGKDSOG 201
QY 181 DSGGPLVNCOSLOGIISWGDPFCATITRRKPGVYTKVCKYVDWIQETMKNN 229
DB 202 DSGGPLVNCOSLOGIISWGDPFCATITRRKPGVYTKVCKYVDWIQETMKNN 250

RESULT 7
ABB95526
ID ABB95526 standard; Protein; 250 AA.
XX
AC ABB95526;
XX
DT 19-JUN-2002 (first entry)
DE Human angiogenesis related protein PRO1279 SEQ ID NO: 208.
XX
KM Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KM atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KM cardiac; cystostatic; antiangiogenic; hypotensive; vulnery;
KM antiarteriosclerotic.
XX
OS Homo sapiens.
XX
PM WO200208284-A2.
XX
PD 31-JAN-2002.
XX
PF 09-JUN-2001; 2001WO-US21735.
XX
PR 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220664P.
PR 28-JUL-2000; 2000WO-US20710.
PR 02-AUG-2000; 2000US-222695P.
PR 17-AUG-2000; 2000US-064357.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 07-SEP-2000; 2000US-230978P.
PR 15-SEP-2000; 2000US-000000P.
PR 18-SEP-2000; 2000US-0665350.
PR 24-OCT-2000; 2000US-242922P.
PR 08-NOV-2000; 2000US-0709238.
PR 10-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 22-JAN-2001; 2001US-0767609.
PR 28-FEB-2001; 2001US-0796498.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001US-US06666.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-080689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 25-MAY-2001; 2001US-0866034.
PR 25-MAY-2001; 2001US-0866034.
PR 30-MAY-2001; 2001US-0870574.
PR 01-JUN-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.

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PR 28-JUN-2001; 2001WO-US00000.
XX
XX (GETH ) GENENTECH INC.
PA (BAKE ) BAKER K P.
PA (FERRA ) FERRARA N.
PA (GERB ) GERBER H.
PA (GERR ) GERRITSEN M E.
PA (GODD ) GODDARD A.
PA (GODO ) GODDARD P J.
PA (GURN ) GURNEY A L.
PA (HILL ) HILLAN K J.
PA (MARS ) MARSTERS S A.
PA (PANJ ) PAN J.
PA (PAON ) PAONI N F.
PA (STEP ) STEPHAN J F.
PA (WATA ) WATANABE C K.
PA (WILL ) WILLIAMS P M.
PA (WOOD ) WOOD W I.
XX
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AU, Hillan KJ, Marsters SA, Pan J, Paoni NF,
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
XX MPI: 2002-171999/22.
DR N-FSDB; ABL95664.
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
XX useful in diagnosis and treatment of cardiovascular (e.g. myocardial
XX infarction), endothelial or angiogenic disorders in a mammal -
XX
XX Claim 11; Fig 208; 567pp; English.
XX
XX The present invention provides the protein and coding sequences of human
XX PRO proteins. These are useful for treating or diagnosing a
XX cardiovascular, endothelial or angiogenic disorder, including cardiac
XX hypertrophy, trauma, cancer, age-related macular degeneration,
XX atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
XX angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
XX angiogenesis (such as breast carcinoma and liver carcinoma) and wound
XX healing. The present sequence is a PRO protein of the invention.
XX
XX Sequence 250 AA;
SQ
Query Match 100.0%; Score 1258; DB 23; Length 250;
Best Local Similarity 100.0%; Pred. No. 6.3e-113;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IIKGFCKPHSQPMOALFEKTRILCGATLAPRMLTAAHCLPKRYIVHLGHNLOKEE 60
DB 22 IIKGFCKPHSQPMOALFEKTRILCGATLAPRMLTAAHCLPKRYIVHLGHNLOKEE 81
QY 61 GCEQRTITATSEFPHPGFNNSLPNKDHNDIMLVKMASPVSTITWAVRPLTSSRCVTAGTS 120
DB 82 GCEQRTITATSEFPHPGFNNSLPNKDHNDIMLVKMASPVSTITWAVRPLTSSRCVTAGTS 141
QY 121 CLISGWSGTSPPQLRPLHTLRCAANTITIEHOKCENAYPGNITDTMVCASVOEGGKDSOG 180
DB 142 CLISGWSGTSPPQLRPLHTLRCAANTITIEHOKCENAYPGNITDTMVCASVOEGGKDSOG 201
QY 181 DSGGPLVNCOSLOGIISWGDPFCATITRRKPGVYTKVCKYVDWIQETMKNN 229
DB 202 DSGGPLVNCOSLOGIISWGDPFCATITRRKPGVYTKVCKYVDWIQETMKNN 250

RESULT 8
ABB84920
ID ABB84920 standard; Protein; 250 AA.
XX
AC ABB84920;
XX
DT 16-MAY-2002 (first entry)
DE Human PRO1279 protein sequence SEQ ID NO:208.

```

XX Human; angiogenesis; cardiant; cytosolic; antiangiogenic; hypotensive;
 KW Vlnary; antarteriosclerotic; PRO agonist; PRO antagonist; trauma;
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 KW angiogenic disorder; cardiac hypertrophy; arteriosclerosis; hypertension;
 KW age-related macular degeneration; arterial restenosis; angina;
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
 KW lymphangitis; tumor angiogenesis; breast carcinoma; liver carcinoma;
 KW wound healing; chromosome mapping; gene mapping.
 XX
 OS Homo sapiens.
 XX
 PN WO200200690-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 20-JUN-2001; 2001WO-US19692.
 XX
 XX 23-JUN-2000; 2000US-213637P.
 PR 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 25-JUL-2000; 2000US-220664P.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 02-AUG-2000; 2000US-222655P.
 PR 17-AUG-2000; 2000US-0643657.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 07-SEP-2000; 2000US-230978P.
 PR 18-SEP-2000; 2000US-0664610.
 PR 18-SEP-2000; 2000US-0665350.
 PR 24-OCT-2000; 2000US-242923P.
 PR 08-NOV-2000; 2000US-0709238.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 22-JAN-2001; 2001US-0767609.
 PR 28-FEB-2001; 2001US-0796498.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0806869.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 30-MAY-2001; 2001US-0870574.
 PR 30-MAY-2001; 2001WO-US17443.
 PR 01-JUN-2001; 2001WO-US17800.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Warsters SA, Pan U, Paoni NF;
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 DR WPI; 2002-090516/12.
 DR N-PSDB; ABL88175.
 XX
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal -
 XX
 PS Claim 11; Fig 208; 565pp; English.
 CC ABL88072 to ABL88258 encode the PRO proteins given in ABL884817 to
 CC ABL885003. The PRO proteins and polynucleotides have cardiant, cytosolic,
 CC antiangiogenic, hypotensive, vlnary and antarteriosclerotic
 CC activities, and can be used in gene therapy. The PRO polynucleotides,

CC proteins, agonists and antagonists are useful for treating or diagnosing
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal.
 CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular
 CC degeneration, arteriosclerosis, hypertension, arterial restenosis,
 CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
 CC lymphangitis, tumor angiogenesis (such as breast carcinoma and liver
 CC carcinoma) and wound healing. The PRO polynucleotides have applications
 CC in molecular biology, including use as hybridisation probes, and in
 CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
 CC probes used in the exemplification of the present invention.
 XX
 XX Sequence 250 AA;
 SQ
 Query Match 100.0%; Score 1258; DB 23; Length 250;
 Best Local Similarity 100.0%; Pred No. 6.3e-113; Mismatches 229; Conservative 0; Indels 0; Gaps 0;
 QY 1 IIKGFCKPSPQWQALFEKTRLLCGATLIPRWLLTAHCLKPRYIVHLGQNLQKEE 60
 DB 22 IIKGFCKPSPQWQALFEKTRLLCGATLIPRWLLTAHCLKPRYIVHLGQNLQKEE 81
 QY 61 GCEQRTATSPPHGFNNSLPNKQHRNDIMLVKASPVSTWAVRPLTSSRCVTAGTS 120
 DB 82 GCEQRTATSPPHGFNNSLPNKQHRNDIMLVKASPVSTWAVRPLTSSRCVTAGTS 141
 QY 121 CLISGSGTSSPOLRLPHTLRCAITIEHOKCENAVPENITDTCWCAVQESGKSCOG 180
 DB 142 CLISGSGTSSPOLRLPHTLRCAITIEHOKCENAVPENITDTCWCAVQESGKSCOG 201
 QY 181 DSGGPLVNCQSLQGIISWGQDPCATTRKPGVYTKYCKYVDWIQETMKN 229
 DB 202 DSGGPLVNCQSLQGIISWGQDPCATTRKPGVYTKYCKYVDWIQETMKN 250
 RESULT 9
 AAU83684
 ID AAU83684 standard; Protein; 250 AA.
 AC AAU83684;
 DT 08-MAY-2002 (first entry)
 DE Human PRO protein, Seq ID No 186.
 KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
 KW breast cancer; prostate tumour; rectal tumour; liver tumour;
 KW pericyte cell proliferation; chondrocyte cell proliferation;
 KW tumour necrosis factor-alpha.
 OS Homo sapiens.
 PN WO200208288-A2.
 PD 31-JAN-2002.
 PF 29-JUN-2001; 2001WO-US21066.
 PR 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220585P.
 PR 25-JUL-2000; 2000US-220605P.
 PR 25-JUL-2000; 2000US-220607P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 25-JUL-2000; 2000US-220638P.
 PR 25-JUL-2000; 2000US-220664P.
 PR 26-JUL-2000; 2000US-220666P.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 15-SEP-2000; 2000US-000000P.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 28-NOV-2000; 2000US-253646P.
 PR 01-DEC-2000; 2000WO-US32678.

PR 20-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001WO-US17092.
XX
PA (GETH) GENENTECH INC.
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ,
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT;
XX
DR MPI; 2002-172001/22.
DR N-PSDB; ARK33628.
XX
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT useful for treating a PRO related disorder and for diagnosing tumours
PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
PT tumour or liver tumour -
XX
PS Claim 11; Figure 186; 359pp; English.
XX
XX The invention relates to one hundred and twenty two nucleic acids
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
CC agonists and antagonists are useful for treating a PRO related disorder.
CC The PRO polypeptides are useful for diagnosing tumours, especially lung
CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. The PRO polypeptides are useful for stimulating the
CC proliferation of, or gene expression, in pericyte cells, for stimulating
CC the proliferation or differentiation of chondrocyte cells, for
CC stimulating the release of tumour necrosis factor-alpha from human blood,
CC for stimulating or inhibiting the proliferation of normal human dermal
CC fibroblast cells. The PRO polypeptide may also be used as molecular
CC weight markers and for tissue typing. The PRO nucleic acids have
CC applications in molecular biology, including use as hybridisation probes,
CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
CC protein sequences of the invention.
XX
XX Sequence 250 AA;
SQ
Query Match 100.0%; Score 1258; DB 23; Length 250;
Best Local Similarity 100.0%; Pred. No. 6,36-113;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IIKGECKPHSQWQALFEKTRLLCGATLIPRLTLTAHCLKRYIVHLGQNLQKEE 60
DB 22 IIKGECKPHSQWQALFEKTRLLCGATLIPRLTLTAHCLKRYIVHLGQNLQKEE 81
QY 61 GCEQRTTATESPPHGFNNSLPNKDRNDIMLVKASVSTTWAVRPLTSSRCTACTS 120
DB 82 GCEQRTTATESPPHGFNNSLPNKDRNDIMLVKASVSTTWAVRPLTSSRCTACTS 141
QY 121 CLISGSGTSSPOLRLPHTLRCANITITIEHOKCEAAYNGNITDTWVCASVOEGKDSQCG 180
DB 142 CLISGSGTSSPOLRLPHTLRCANITITIEHOKCEAAYNGNITDTWVCASVOEGKDSQCG 201
QY 181 DSGGELVNCQSLQGIISWGQDPCATTRKPGYTVKVCYVDWIQETMKXN 229
DB 202 DSGGELVNCQSLQGIISWGQDPCATTRKPGYTVKVCYVDWIQETMKXN 250
RESULT 10
ABU66822
ID ABU66822 standard; Protein; 250 AA.
XX
XX ABU66822;
XX
XX 23-MAY-2003 (first entry)
XX
XX Human PRO polypeptide #253.
XX
XX Human; PRO polypeptide; secreted and transmembrane protein;
KW -tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;

KW differentiation; chondrocyte; tumour; genetic disorder;
KW cytosolic.
XX
XX Homo sapiens.
XX
XX US2003036180-A1.
XX
XX 20-FEB-2003.
XX
XX 09-MAY-2002; 2002US-0143114.
XX
XX 31-MAR-1997; 97WO-US05230.
PR 12-JUN-1998; 98WO-US12456.
PR 14-JUL-1998; 98WO-US14552.
PR 28-AUG-1998; 98WO-US17888.
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19093.
PR 14-SEP-1998; 98WO-US19094.
PR 14-SEP-1998; 98WO-US19177.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 29-OCT-1998; 98WO-US22991.
PR 29-OCT-1998; 98WO-US22992.
PR 20-NOV-1998; 98WO-US24855.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99WO-US05190.
PR 20-APR-1999; 99WO-US08615.
PR 14-MAY-1999; 99WO-US10723.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28409.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 22-DEC-1999; 99WO-US30720.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US0376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05746.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15254.

28-JUL-2000; 2000WO-US20710.
 PR 11-AUG-2000; 2000WO-US22031.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 22-JUN-2001; 2001WO-US20116.
 PR 29-JUN-2001; 2001WO-US21066.
 PR 09-JUL-2001; 2001WO-US21735.
 PR 20-DEC-2000; 2000US-0747259.
 PR 28-FEB-2001; 2001US-0796498.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0808689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 18-MAY-2001; 2001US-0860216.
 PR 25-MAY-2001; 2001US-0866034.
 PR 01-JUN-2001; 2001US-0872035.
 PR 05-JUN-2001; 2001US-0874503.
 PR 14-JUN-2001; 2001US-0882636.
 PR 19-JUN-2001; 2001US-0886342.
 PR 21-JUN-2001; 2001US-0887879.
 PR 18-JUL-2001; 2001US-0908827.
 PR 06-AUG-2001; 2001US-0924419.
 PR 09-AUG-2001; 2001US-0927796.
 PR 16-AUG-2001; 2001US-0931836.
 PR 19-DEC-2001; 2001US-0028072.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Beresini M, DeForge L, Deenoyers L, Filvaroff E, Gao W,
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 DR WPI; 2003-332040/31.
 DR N-PSDB; ACA03855.
 XX New secreted and transmembrane PRO nucleic acids, useful for gene
 PT therapy, in chromosome and gene mapping, as chromosome markers, in
 PT tissue typing, and in chromosome identification
 XX
 XX Claim 12; Fig 506; 660pp; English.
 XX The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The PRO
 CC polypeptides are useful for detecting other PRO polypeptides, for
 CC linking bioactive molecules to cells expressing PRO polypeptides,
 CC for modulating biological activities of cells expressing PRO
 CC polypeptides, and for identifying agonists or antagonists.
 CC The PRO polypeptides are useful for stimulating the release of
 CC tumour necrosis factor (TNF)-alpha from human blood, for stimulating
 CC the proliferation or differentiation of chondrocytes, and detecting the
 CC presence of tumours. The polynucleotide sequences encoding PRO
 CC polypeptides are useful as hybridisation probes, in chromosome and
 CC gene mapping, in the generation of antisense RNA and DNA, in the
 CC preparation of PRO polypeptides, for generating transgenic animals or
 CC knockout animals, for the genetic analysis of individuals with genetic
 CC disorders, and in gene therapy. AB06570-AB066844 represent the human
 CC PRO polypeptides of the invention.
 CC Note: The sequence data for this patent was obtained in electronic
 CC format directly from the USPTO web site at
 CC seqdata.uspto.gov/psipdsidentry.html.

XX
 SQ Sequence 250 AA;
 Query Match 100.0%; Score 1258; DB 24; Length 250;
 Best Local Similarity 100.0%; Pred. No. 6.3e-113;
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IIKGFECRHSOPWQALAEKTRLLCGATLLIAPRWLLTTAAHCLKPRYIYHLCGHNLQKEE 60
 DB 22 IIKGFECRHSOPWQALAEKTRLLCGATLLIAPRWLLTTAAHCLKPRYIYHLCGHNLQKEE 81
 QY 61 GCEOTRTATESFPHPFNNSLPNKDHRNDIMEVKMSPSITWAVPPLTSSRCVTAGTS 120
 DB 82 GCEOTRTATESFPHPFNNSLPNKDHRNDIMEVKMSPSITWAVPPLTSSRCVTAGTS 141
 DB 142 CLISGWSTSSPOLRLPHTLRCAANTIIEHOKCENAYPGNITDTWVCASVQEGKDCSCG 201
 QY 121 CLISGWSTSSPOLRLPHTLRCAANTIIEHOKCENAYPGNITDTWVCASVQEGKDCSCG 180
 DB 142 CLISGWSTSSPOLRLPHTLRCAANTIIEHOKCENAYPGNITDTWVCASVQEGKDCSCG 201
 QY 181 DSGGPLVCNOSLOGIISWGQDCATRRKPGVYTKCKYVDWIQETMKN 229
 DB 202 DSGGPLVCNOSLOGIISWGQDCATRRKPGVYTKCKYVDWIQETMKN 250
 RESULT 11
 AB067098
 ID AB067098 standard; Protein; 250 AA.
 XX
 AC AB067098;
 XX
 DT 27-MAY-2003 (first entry)
 XX
 DE Human secreted/transmembrane, PRO, protein SEQ ID 506.
 XX
 XX Human; secreted protein; transmembrane protein; PRO;
 KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;
 KW infertility; birth defects; premature aging; AIDS; biosensor;
 KW acquired immunodeficiency syndrome; cancer; diabetic complication;
 KW bioreactor; tumour.
 XX
 XX Homo sapiens.
 OS
 XX
 PN US2003032155-A1.
 XX
 PD 13-FEB-2003.
 XX
 PF 03-MAY-2002; 2002US-0137865.
 XX
 PR 31-MAR-1997; 97WO-US05230.
 PR 12-JUN-1998; 98WO-US12456.
 PR 14-JUL-1998; 98WO-US14552.
 PR 28-AUG-1998; 98WO-US17888.
 PR 10-SEP-1998; 98WO-US18824.
 PR 14-SEP-1998; 98WO-US19093.
 PR 14-SEP-1998; 98WO-US19094.
 PR 14-SEP-1998; 98WO-US19177.
 PR 16-SEP-1998; 98WO-US19330.
 PR 17-SEP-1998; 98WO-US19437.
 PR 07-OCT-1998; 98WO-US21141.
 PR 29-OCT-1998; 98WO-US22991.
 PR 29-OCT-1998; 98WO-US22992.
 PR 20-NOV-1998; 98WO-US24855.
 PR 01-DEC-1998; 98WO-US25108.
 PR 05-JAN-1999; 99WO-US00106.
 PR 08-MAR-1999; 99WO-US05028.
 PR 10-MAR-1999; 99WO-US05190.
 PR 20-APR-1999; 99WO-US08615.
 PR 14-MAY-1999; 99WO-US10733.
 PR 02-JUN-1999; 99WO-US12252.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 13-SEP-1999; 99WO-US20944.
 PR 15-SEP-1999; 99WO-US21090.

PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28409.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30991.
PR 20-DEC-1999; 99WO-US30999.
PR 22-DEC-1999; 99WO-US30720.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05746.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US14705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22321.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 22-JUN-2001; 2001WO-US20116.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 20-DEC-2000; 2000WO-US27259.
PR 28-FEB-2001; 2001US-0796498.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-080689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 18-MAY-2001; 2001US-0860216.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 21-JUN-2001; 2001US-0887879.
PR 18-JUL-2001; 2001US-0908827.
PR 06-AUG-2001; 2001US-0924419.
PR 09-AUG-2001; 2001US-0927796.
PR 16-AUG-2001; 2001US-0931836.

PR 19-DEC-2001; 2001US-0028072.
XX (GETH) GENENTECH INC.
PA Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
XX Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Geritsen ME, Stewart VA, Tumas D, Watanabe CK, Wood WL, Zhang Z;
PI Smith V, WPI, 2003-331925/31.
XX N-PSDB; ACA04276.
DR New secreted and transmembrane nucleic acids and polypeptides,
XX designated as PRO, useful for treating inflammation, organ failure,
PT atherosclerosis, cardiac injury, infertility, birth defects, premature
PT aging, AIDS, or cancer
XX
PS Claim 12; Fig 506; 659pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising, or which is
CC at least 80% identical to, or the full-length coding sequence of, any of
CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
CC (one of 275 secreted or transmembrane proteins). The nucleic acid
CC further comprises the full-length coding sequence of the DNA deposited
CC under American Type Culture Collection (ATCC) accession number in a list
CC given in the specification. Also included are vectors and host
CC cells for producing PRO proteins, PRO fusion proteins, anti-PRO
CC antibodies, PRO extracellular domains and mature sequences, methods
CC of detecting PRO proteins, methods for stimulating the release of
CC TNF-alpha (tumour necrosis factor alpha) from human blood,
CC (and the proliferation of differentiation of chondrocyte cells, the
CC proliferation of, or gene expression in pericyte cells, the release or
CC proteoglycans from cartilage, proliferation of inner ear utricular
CC supporting cells, the proliferation of T-lymphocyte cells, the release
CC of a cytokine from peripheral blood mononuclear cells (PBMC), or the
CC proliferation of endothelial cells), a method for modulating the uptake
CC of glucose or free fatty acid (FFA) by skeletal muscle cells,
CC a method for inhibiting the binding of A-peptide to factor VIIa,
CC or the differentiation of adipocyte cells, a method for detecting the
CC presence of a tumour in a mammal and an oligonucleotide probe derived
CC from any of the nucleotide sequences cited above. The nucleic acids and
CC polypeptides are useful for treating inflammatory diseases, organ
CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
CC premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or
CC diabetic complications. The nucleic acids are useful as hybridisation
CC probes, in chromosome and gene mapping, and in generating antisense RNA
CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,
CC biosensors or bioreactors. Both are useful in tissue typing.
XX The present sequence represents a PRO protein of the invention.
XX
SQ Sequence 250 AA;
Query Match 100.0%; Score 1256; DB 24; Length 250;
Best Local Similarity 100.0%; Pred. No. 6.3e-113;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IIKGECKPHQPOALFEKTRLLCGATLAPRWLTAACHLPRIYVHNGHNLQEE 60
DB 22 IIKGECKPHQPOALFEKTRLLCGATLAPRWLTAACHLPRIYVHNGHNLQEE 81
QY 61 GCEOTRTATESFPHPGFNSLIPNKDRNDIMLVMAASVSIITWAVRPLTLSSRCTACTS 120
DB 82 GCEOTRTATESFPHPGFNSLIPNKDRNDIMLVMAASVSIITWAVRPLTLSSRCTACTS 141
QY 121 CLISGWSSTSSPOLRLPHTLCANITIIHOKCENAVPGNITDTMVCASVOEGGKDCOG 180
DB 142 CLISGWSSTSSPOLRLPHTLCANITIIHOKCENAVPGNITDTMVCASVOEGGKDCOG 201
QY 181 DSGGPLVNCOSLQGIISWGDPICATIRKPGVYTVCKYVDVIOETMKN 229
DB 202 DSGGPLVNCOSLQGIISWGDPICATIRKPGVYTVCKYVDVIOETMKN 250
RESULT 12

ABUS9903
ID ABUS9903 standard; Protein; 250 AA.
XX
AC ABUS9903;
XX
DT 13-MAY-2003 (first entry)
XX
DE Novel secreted and transmembrane protein PRO1279.
XX
KW Human; PRO: hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosa; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis.
XX
OS Homo sapiens.
XX
PN US2003017563-A1.
XX
PD 23-JAN-2003.
XX
PF 07-MAY-2002; 2002US-0140808.
XX
XX 31-MAR-1997; 97WO-US05330.
PR 12-JUN-1998; 98WO-US12456.
PR 14-JUL-1998; 98WO-US14552.
PR 28-AUG-1998; 98WO-US17888.
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19093.
PR 14-SEP-1998; 98WO-US19094.
PR 14-SEP-1998; 98WO-US19177.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 29-OCT-1998; 98WO-US22891.
PR 29-OCT-1998; 98WO-US22992.
PR 20-NOV-1998; 98WO-US24855.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US05106.
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99WO-US05190.
PR 20-APR-1999; 99WO-US08615.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28409.
PR 01-DEC-1999; 99WO-US28310.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28651.
PR 02-DEC-1999; 99WO-US28664.
PR 02-DEC-1999; 99WO-US28665.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 22-DEC-1999; 99WO-US30720.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.

PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05746.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US18692.
PR 22-JUN-2001; 2001WO-US20116.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 20-DEC-2000; 2000US-0747259.
PR 28-FEB-2001; 2001US-0796498.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0815744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 18-MAY-2001; 2001US-0854280.
PR 18-MAY-2001; 2001US-0860216.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 01-JUN-2001; 2001US-0865035.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 21-JUN-2001; 2001US-0887879.
PR 18-JUL-2001; 2001US-0908827.
PR 06-AUG-2001; 2001US-0924419.
PR 09-AUG-2001; 2001US-0927796.
PR 16-AUG-2001; 2001US-0931836.
PR 19-DEC-2001; 2001US-0028072.
XX
PA (GENTECH) GENENTECH INC.
XX
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W,
PI Gerlitsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S,
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WJ, Zhang Z,
XX
DR WPI; 2003-148238/14.
DR N-PSDB; ABX89393.
XX
XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT are therapeutically useful for enhancing immune response and in cancer
PT treatments -
XX
XX Claim 12; Fig 506; 659pp; English.
PS
XX The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting human PRO polypeptides in a sample, in

CC Linking a bioactive molecule to a cell expressing a PRO polypeptide, and
 CC in modulating at least one biological activity of a cell expressing a PRO
 CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
 CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
 CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
 CC PRO943, PRO828, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
 CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
 CC useful for treating conditions or disorders where angiogenesis would be
 CC beneficial, e.g. wound healing and antagonist of this polypeptide are
 CC useful for treating cancerous tumours. PRO812 inhibits vascular
 CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
 CC cells and is thus useful for inhibiting endothelial cell growth in
 CC mammals which would be beneficial in inhibiting tumour growth. PRO26,
 CC PRO1068, PRO1184, PRO1366 and PRO1375 stimulate proliferation of
 CC stimulated T-lymphocytes and are therapeutically useful for enhancing
 CC immune response. PRO826, PRO1068 or PRO1132 enhance survival of
 CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
 CC rod photoreceptor cells) and therefore are useful for treating retinal
 CC disorders of injuries, e.g. retinitis pigmentosa, AMP. PRO819, PRO813
 CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
 CC and therefore are useful for treating kidney disorders associated with
 CC decreased mesangial cell function such as Berger disease or Crohn's
 CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
 CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
 CC proliferation and/or redifferentiation of chondrocytes in culture and
 CC are thus useful for treating sports injuries, and arthritis. This
 CC is the amino acid sequence of a novel human PRO protein.

SO Sequence 250 AA;

Query Match 100.0%; Score 1258; DB 24; Length 250;
 Best Local Similarity 100.0%; Pred. No. 6.3e-113;
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IIKGECKPSPQWQALFEKTRLLCGATLAPRWMLTAHCLKPRIVYHVGQNLQKEE 60
 DB 22 IIKGECKPSPQWQALFEKTRLLCGATLAPRWMLTAHCLKPRIVYHVGQNLQKEE 81
 OY 61 GCEQTRTATESFPHPGNNNSLPNKHNDIMLVKMASPVSIITMAVRPLTSSRCVTAGTS 120
 DB 82 GCEQTRTATESFPHPGNNNSLPNKHNDIMLVKMASPVSIITMAVRPLTSSRCVTAGTS 141
 OY 121 CLISGWSSTSPQLRLPHTLRCAANTITIEHOKCENAYPGNITDTMVCASVOEGKDSQCG 180
 DB 142 CLISGWSSTSPQLRLPHTLRCAANTITIEHOKCENAYPGNITDTMVCASVOEGKDSQCG 201
 OY 181 DSGGPLVNCNOSLQGIISWGODPCAITRKPGVYTKVKCYVDVIOETMKN 229
 DB 202 DSGGPLVNCNOSLQGIISWGODPCAITRKPGVYTKVKCYVDVIOETMKN 250

RESULT 13

ABUS6739 standard; Protein; 250 AA.

AC ABUS6739;

DT 02-APR-2003 (first entry)

DE Lung cancer-associated polypeptide #332.

KW Lung cancer-associated polypeptide; cytostatic; emphysema;
 KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
 KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
 KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
 KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

OS Unidentified.

XX WO200286443-A2.

XX 31-OCT-2002.

XX

PF 18-APR-2002; 2002WO-US12476.
 XX 18-APR-2001; 2001US-284770P.
 PR 10-MAY-2001; 2001US-290492P.
 PR 09-NOV-2001; 2001US-339245P.
 PR 13-NOV-2001; 2001US-350666P.
 PR 29-NOV-2001; 2001US-334370P.
 PR 12-APR-2002; 2002US-372246P.
 XX (EOSB-) EOS BIOTECHNOLOGY INC.
 PA Aziz N, Murray R;
 PI WPI; 2003-093161/08.
 DR N-PSDB; ABX76468.
 XX
 PT Detecting a lung cancer-associated transcript in a cell from a patient
 PT for treating lung cancer, by contacting a biological sample from the
 PT patient with a polynucleotide that exhibits increased or decreased
 PT expression in lung cancer -
 XX
 XX Claim 27; Page 443-444; 453pp; English.

CC The invention relates to a method for detecting a lung cancer-associated
 CC transcript in a cell from a patient, comprising contacting a biological
 CC sample from the patient with a polynucleotide that selectively hybridises
 CC to a sequence that is at least 80 % identical to a gene that exhibits
 CC increased or decreased expression in lung cancer samples. Lung
 CC cancer-associated polynucleotides and polypeptides are used for
 CC identifying a compound that modulates a lung cancer-associated
 CC polypeptide, for inhibiting proliferation of a lung cancer-associated
 CC cell to treat lung cancer in a patient and for treating a mammal having
 CC lung cancer by administering a modulatory compound identified. The
 CC methods are useful for treating lung cancer, such as small cell lung
 CC cancer, non-small cell lung cancer or other benign or precancerous
 CC lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive
 CC pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial
 CC pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides
 CC and polypeptides are useful for diagnostic purposes and as targets for
 CC screening for therapeutic compounds that modulate lung cancer, such as
 CC antibodies. Sequences ABUS6408-ABUS6745 represent lung cancer-associated
 CC polypeptides of the invention.

XX Sequence 250 AA;

Query Match 100.0%; Score 1258; DB 24; Length 250;
 Best Local Similarity 100.0%; Pred. No. 6.3e-113;
 Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IIKGECKPSPQWQALFEKTRLLCGATLAPRWMLTAHCLKPRIVYHVGQNLQKEE 60
 DB 22 IIKGECKPSPQWQALFEKTRLLCGATLAPRWMLTAHCLKPRIVYHVGQNLQKEE 81
 OY 61 GCEQTRTATESFPHPGNNNSLPNKHNDIMLVKMASPVSIITMAVRPLTSSRCVTAGTS 120
 DB 82 GCEQTRTATESFPHPGNNNSLPNKHNDIMLVKMASPVSIITMAVRPLTSSRCVTAGTS 141
 OY 121 CLISGWSSTSPQLRLPHTLRCAANTITIEHOKCENAYPGNITDTMVCASVOEGKDSQCG 180
 DB 142 CLISGWSSTSPQLRLPHTLRCAANTITIEHOKCENAYPGNITDTMVCASVOEGKDSQCG 201
 OY 181 DSGGPLVNCNOSLQGIISWGODPCAITRKPGVYTKVKCYVDVIOETMKN 229
 DB 202 DSGGPLVNCNOSLQGIISWGODPCAITRKPGVYTKVKCYVDVIOETMKN 250

RESULT 14

AA42439 standard; Protein; 282 AA.

XX AA42439;

DT 08-DEC-1999 (first entry)

```

XX  CASB12 amino acid sequence.
DE
XX
XX  neurospain; cancer; assay; inhibitor; serine protease; immunogenic;
KM  autoimmune disease.
XX
XX  Homo sapiens.
OS
XX  WO9949055-A1.
PN
XX  30-SEP-1999.
PD
XX  17-MAR-1999; 99WO-EP01894.
PF
XX  20-MAR-1998; 98GB-0006095.
PR
XX
XX  (SMK ) SMITHKLINE BEECHAM BIOLOGICALS.
PA
XX  Bruck CEM, Caesart J, Coche T, Vinals-bassols C;
PI
XX  WPI; 1999-580450/49.
DR
XX  N-PSDB; AA222638.
DR
XX
XX  New human serine protease CASB12, for treatment, prevention and
PT  diagnosis of cancer and autoimmune diseases
PT
XX
XX  Claim 3; Page 48; 58pp; English.
PS
XX
XX  This is the amino acid sequence of the CASB12 protein. The nucleotide
CC  sequence of AA222638 shows homology with neurospain and the encoded
CC  protein AA42439 is structurally related to other proteins of the
CC  serine protease family, having homology and/or structural similarity
CC  with neurospain. It is expected that as well as similar structure, these
CC  proteins will also share similar biological functions and properties.
CC  The CASB12 polypeptides and polynucleotides can be used to develop
CC  methods for identifying agonists and antagonists/inhibitors of these
CC  molecules, and thereby treating conditions associated with CASB12
CC  polypeptide imbalance. The invention also provides for diagnostic assays
CC  for detecting diseases associated with inappropriate CASB12 polypeptide
CC  activity or levels.
CC  Since CASB12 is either specifically expressed or highly over-expressed
CC  in tumors compared to normal cells, the polypeptides and polynucleotides
CC  of the invention are believed to be important immunogens for specific
CC  prophylactic or therapeutic immunization against tumors. The
CC  polypeptides and polynucleotides can therefore be targeted by antigen
CC  specific immune reactions (which result in the destruction of the tumor
CC  cell) or they can be used to diagnose the occurrence of tumor cells
CC
XX
XX  Sequence 282 AA;
SQ
Query Match 100.0%; Score 1258; DB 20; Length 282;
Best Local Similarity 100.0%; Pred. No. 7.4e-113;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IIKGFECKPHSQPWOALFEKTRILCGATLIPRMLTAAHCLKPRYIVHLCQHNLOKXE 60
DB 54 IIKGFECKPHSQPWOALFEKTRILCGATLIPRMLTAAHCLKPRYIVHLCQHNLOKXE 113
QY 61 GCEQRTATSEFPHPGFNNSLPNKDHRNDIMLVKASPVSTWAVRPLTLSSRCTACTS 120
DB 114 GCEQRTATSEFPHPGFNNSLPNKDHRNDIMLVKASPVSTWAVRPLTLSSRCTACTS 173
QY 121 CLISGSGTSSPOLRPLHTLRCAANTIIIEHOKCENAYPGNITDWTWCASVOEGKDSGCG 180
DB 174 CLISGSGTSSPOLRPLHTLRCAANTIIIEHOKCENAYPGNITDWTWCASVOEGKDSGCG 233
QY 181 DSGGPLVNCQSLQGIISWQDPCATIRKPGVYTKYCKYVDWIQETMKNN 229
DB 234 DSGGPLVNCQSLQGIISWQDPCATIRKPGVYTKYCKYVDWIQETMKNN 282
RESULT 15
AAB11712

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```

ID  AAB11712 standard; Protein; 282 AA.
XX
XX  AAB11712;
AC
XX
XX  23-OCT-2000 (first entry)
DT
XX
XX  Human serine protease BSSP6 (hBSSP6) SEQ ID NO:2.
DE
XX
XX  BSSP6; serine protease; human; hBSSP6; mouse; mBSSP6; brain;
KM  diagnostic marker; antibody; transgenic animal; Alzheimer's disease;
KM  epilepsy; cancer; inflammation; infertility; pancreatitis;
KM  prostatic hypertrophy.
XX
XX  Homo sapiens.
OS
XX  WO200031257-A1.
PN
XX  02-JUN-2000.
PD
XX  19-NOV-1999; 99WO-JP06476.
PF
XX  20-NOV-1998; 98JP-0347802.
PR
XX
XX  (FUSO ) FUSO PHARM IND LTD.
PA
XX
XX  Uemura H, Okui A, Kominami K, Yamaguchi N, Mitsu S;
PI
XX  WPI, 2000-400067/34.
DR
XX  N-PSDB; AAA61763.
DR
XX
XX  Serine protease BSSP6, useful in detecting homologs, mutants and
PT  polymorphic variants as markers for diagnosis of Alzheimer's disease,
PT  epilepsy, cancer, inflammation, infertility and prostatic hypertrophy,
PT  using blood or other tissues
XX
XX  Claim 1; Page 69-70; 94pp; Japanese.
PS
XX
XX  The invention relates to novel serine proteases designated BSSP6
CC  (AAB11712-B11714), and to nucleic acids encoding them (AAA61763-A61765).
CC  The invention also relates to vectors and transformants comprising BSSP6
CC  nucleic acids; transgenic animals in which the expression level of BSSP6
CC  can be varied; and an mBSSP6 knockout mouse. The invention additionally
CC  encompasses anti-BSSP6 antibodies and methods of production of such
CC  antibodies, methods of BSSP6 detection using the antibodies, and the
CC  use of BSSP6 proteins or fragments as diagnostic markers for certain
CC  medical conditions. Nucleotides encoding BSSP6 were initially
CC  isolated in a human brain cDNA library using degenerate PCR primers
CC  (AAA61795-A61796) based on conserved regions of serine proteases. The
CC  BSSP6 serine proteases and nucleotides encoding them are useful in
CC  detecting homologues, mutants and polymorphic variants in biological
CC  samples (e.g., blood, urine, brain, prostate gland, placenta, testis
CC  and spleen) as diagnostic markers for conditions such as Alzheimer's
CC  disease, epilepsy, cancer, inflammation, infertility and prostatic
CC  hypertrophy. Sequences AAB11712 and AAB11714 represent human BSSP6
CC  variants (hBSSP6), and sequence AAB11713 represents murine BSSP6
CC  (mBSSP6).
XX
XX  Sequence 282 AA;
SQ
Query Match 100.0%; Score 1258; DB 21; Length 282;
Best Local Similarity 100.0%; Pred. No. 7.4e-113;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IIKGFECKPHSQPWOALFEKTRILCGATLIPRMLTAAHCLKPRYIVHLCQHNLOKXE 60
DB 54 IIKGFECKPHSQPWOALFEKTRILCGATLIPRMLTAAHCLKPRYIVHLCQHNLOKXE 113
QY 61 GCEQRTATSEFPHPGFNNSLPNKDHRNDIMLVKASPVSTWAVRPLTLSSRCTACTS 120
DB 114 GCEQRTATSEFPHPGFNNSLPNKDHRNDIMLVKASPVSTWAVRPLTLSSRCTACTS 173
QY 121 CLISGSGTSSPOLRPLHTLRCAANTIIIEHOKCENAYPGNITDWTWCASVOEGKDSGCG 180

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Db	174	CLISGWSTSSPOLRLPHTLRCANITITIEHOKCENAYPGNITDTMVCASVQEGKDCOG	233
Qy	181	DSGGPLVCNQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKN	229
Db	234	DSGGPLVCNQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKN	282

Search completed: October 22, 2003, 15:51:34
 Job time : 35.0587 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2003, 15:50:17 : Search time 21.9589 seconds
(without alignments)
1746.375 Million cell updates/sec

Title: US-09-856-320A-2_COPY_54_282

Perfect score: 1258
Sequence: 1 IIKGFCECKHSPQWQALPE.....GYTVKCYVDMIQETMKNN 229

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 629382 seqs, 167460630 residues

Total number of hits satisfying chosen parameters: 629382

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

1:	/cgn2_6/ptodata/2/pubppa/US07_PUBCOMB.pep.*
2:	/cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pep.*
3:	/cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pep.*
4:	/cgn2_6/ptodata/2/pubppa/US06_PUBCOMB.pep.*
5:	/cgn2_6/ptodata/2/pubppa/US07_NEW_PUB.pep.*
6:	/cgn2_6/ptodata/2/pubppa/US08_PUBCOMB.pep.*
7:	/cgn2_6/ptodata/2/pubppa/US08_NEW_PUB.pep.*
8:	/cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep.*
9:	/cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep.*
10:	/cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep.*
11:	/cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep.*
12:	/cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep.*
13:	/cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep.*
14:	/cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep.*
15:	/cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep.*
16:	/cgn2_6/ptodata/2/pubppa/US10_NEW_PUB.pep.*
17:	/cgn2_6/ptodata/2/pubppa/US10_NEW_PUB.pep.*
18:	/cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1258	100.0	250	11	US-09-946-374-170 Sequence 170, App
2	1258	100.0	250	12	US-10-015-387A-170 Sequence 170, App
3	1258	100.0	250	12	US-10-137-870-506 Sequence 506, App
4	1258	100.0	250	12	US-10-140-018-506 Sequence 506, App
5	1258	100.0	250	12	US-10-140-021-506 Sequence 506, App
6	1258	100.0	250	12	US-10-140-274-506 Sequence 506, App
7	1258	100.0	250	12	US-10-140-471-506 Sequence 506, App
8	1258	100.0	250	12	US-10-140-807-506 Sequence 506, App
9	1258	100.0	250	12	US-10-140-922-506 Sequence 506, App
10	1258	100.0	250	12	US-10-140-924-506 Sequence 506, App
11	1258	100.0	250	12	US-10-140-926-506 Sequence 506, App
12	1258	100.0	250	12	US-10-141-698-506 Sequence 506, App
13	1258	100.0	250	12	US-10-141-702-506 Sequence 506, App
14	1258	100.0	250	12	US-10-141-704-506 Sequence 506, App
15	1258	100.0	250	12	US-10-142-421-506 Sequence 506, App

16	1258	100.0	250	12	US-10-142-432-506 Sequence 506, App
17	1258	100.0	250	12	US-10-142-767-506 Sequence 506, App
18	1258	100.0	250	12	US-10-143-033-506 Sequence 506, App
19	1258	100.0	250	12	US-10-144-994-506 Sequence 506, App
20	1258	100.0	250	12	US-10-145-628-506 Sequence 506, App
21	1258	100.0	250	12	US-10-145-631-506 Sequence 506, App
22	1258	100.0	250	12	US-10-145-633-506 Sequence 506, App
23	1258	100.0	250	12	US-10-145-746-506 Sequence 506, App
24	1258	100.0	250	12	US-10-145-748-506 Sequence 506, App
25	1258	100.0	250	12	US-10-145-823-506 Sequence 506, App
26	1258	100.0	250	12	US-10-145-826-506 Sequence 506, App
27	1258	100.0	250	12	US-10-145-870-506 Sequence 506, App
28	1258	100.0	250	12	US-10-145-876-506 Sequence 506, App
29	1258	100.0	250	12	US-10-145-959-506 Sequence 506, App
30	1258	100.0	250	12	US-10-146-724-506 Sequence 506, App
31	1258	100.0	250	12	US-10-146-725-506 Sequence 506, App
32	1258	100.0	250	12	US-10-146-795-506 Sequence 506, App
33	1258	100.0	250	12	US-10-147-495-506 Sequence 506, App
34	1258	100.0	250	12	US-10-147-501-506 Sequence 506, App
35	1258	100.0	250	12	US-10-147-504-506 Sequence 506, App
36	1258	100.0	250	12	US-10-147-506-506 Sequence 506, App
37	1258	100.0	250	12	US-10-147-509-506 Sequence 506, App
38	1258	100.0	250	12	US-10-147-510-506 Sequence 506, App
39	1258	100.0	250	12	US-10-147-511-506 Sequence 506, App
40	1258	100.0	250	12	US-10-147-529-506 Sequence 506, App
41	1258	100.0	250	12	US-10-152-397-506 Sequence 506, App
42	1258	100.0	250	12	US-10-153-586-506 Sequence 506, App
43	1258	100.0	250	12	US-10-158-783-506 Sequence 506, App
44	1258	100.0	250	12	US-10-158-786-506 Sequence 506, App
45	1258	100.0	250	12	US-10-006-130A-170 Sequence 170, App

ALIGNMENTS

RESULT 1
US-09-946-374-170
Sequence 170, Application US/09946374
Publication No. US20030073129A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2830P1
CURRENT APPLICATION NUMBER: US/09/946.374
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098749
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098750

1	PRIOR FILING DATE: 1998-09-01
2	PRIOR APPLICATION NUMBER: 60/098803
3	PRIOR FILING DATE: 1998-09-02
4	PRIOR APPLICATION NUMBER: 60/098821
5	PRIOR FILING DATE: 1998-09-02
6	PRIOR APPLICATION NUMBER: 60/098843
7	PRIOR FILING DATE: 1998-09-02
8	PRIOR APPLICATION NUMBER: 60/099536
9	PRIOR FILING DATE: 1998-09-09
10	PRIOR APPLICATION NUMBER: 60/099596
11	PRIOR FILING DATE: 1998-09-09
12	PRIOR APPLICATION NUMBER: 60/099598
13	PRIOR FILING DATE: 1998-09-09
14	PRIOR APPLICATION NUMBER: 60/099602
15	PRIOR FILING DATE: 1998-09-09
16	PRIOR APPLICATION NUMBER: 60/099642
17	PRIOR FILING DATE: 1998-09-09
18	PRIOR APPLICATION NUMBER: 60/099741
19	PRIOR FILING DATE: 1998-09-10
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21	PRIOR FILING DATE: 1998-09-10
22	PRIOR APPLICATION NUMBER: 60/099763
23	PRIOR FILING DATE: 1998-09-10
24	PRIOR APPLICATION NUMBER: 60/099792
25	PRIOR FILING DATE: 1998-09-10
26	PRIOR APPLICATION NUMBER: 60/099808
27	PRIOR FILING DATE: 1998-09-10
28	PRIOR APPLICATION NUMBER: 60/099812
29	PRIOR FILING DATE: 1998-09-10
30	PRIOR APPLICATION NUMBER: 60/099815
31	PRIOR FILING DATE: 1998-09-10
32	PRIOR APPLICATION NUMBER: 60/099816
33	PRIOR FILING DATE: 1998-09-10
34	PRIOR APPLICATION NUMBER: 60/100385
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36	PRIOR APPLICATION NUMBER: 60/100388
37	PRIOR FILING DATE: 1998-09-15
38	PRIOR APPLICATION NUMBER: 60/100390
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40	PRIOR APPLICATION NUMBER: 60/100584
41	PRIOR FILING DATE: 1998-09-16
42	PRIOR APPLICATION NUMBER: 60/100627
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46	PRIOR APPLICATION NUMBER: 60/100662
47	PRIOR FILING DATE: 1998-09-16
48	PRIOR APPLICATION NUMBER: 60/100664
49	PRIOR FILING DATE: 1998-09-16
50	PRIOR APPLICATION NUMBER: 60/100683
51	PRIOR FILING DATE: 1998-09-17
52	PRIOR APPLICATION NUMBER: 60/100684
53	PRIOR FILING DATE: 1998-09-17
54	PRIOR APPLICATION NUMBER: 60/100710
55	PRIOR FILING DATE: 1998-09-17
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73	PRIOR FILING DATE: 1998-09-22

1	PRIOR APPLICATION NUMBER: 60/101471
2	PRIOR FILING DATE: 1998-09-23
3	PRIOR APPLICATION NUMBER: 60/1101472
4	PRIOR FILING DATE: 1998-09-23
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9	PRIOR APPLICATION NUMBER: 60/101476
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11	PRIOR APPLICATION NUMBER: 60/101477
12	PRIOR FILING DATE: 1998-09-23
13	PRIOR APPLICATION NUMBER: 60/101479
14	PRIOR FILING DATE: 1998-09-23
15	PRIOR APPLICATION NUMBER: 60/101738
16	PRIOR FILING DATE: 1998-09-24
17	PRIOR APPLICATION NUMBER: 60/101741
18	PRIOR FILING DATE: 1998-09-24
19	PRIOR APPLICATION NUMBER: 60/101743
20	PRIOR FILING DATE: 1998-09-24
21	PRIOR APPLICATION NUMBER: 60/101915
22	PRIOR FILING DATE: 1998-09-24
23	PRIOR APPLICATION NUMBER: 60/101916
24	PRIOR FILING DATE: 1998-09-24
25	PRIOR APPLICATION NUMBER: 60/102207
26	PRIOR FILING DATE: 1998-09-25
27	PRIOR APPLICATION NUMBER: 60/102244
28	PRIOR FILING DATE: 1998-09-25
29	PRIOR APPLICATION NUMBER: 60/102307
30	PRIOR FILING DATE: 1998-09-25
31	PRIOR APPLICATION NUMBER: 60/102330
32	PRIOR FILING DATE: 1998-09-25
33	PRIOR APPLICATION NUMBER: 60/102333
34	PRIOR FILING DATE: 1998-09-25
35	PRIOR APPLICATION NUMBER: 60/102488
36	PRIOR FILING DATE: 1998-09-30
37	PRIOR APPLICATION NUMBER: 60/102487
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46	PRIOR FILING DATE: 1998-10-01
47	PRIOR APPLICATION NUMBER: 60/102965
48	PRIOR FILING DATE: 1998-10-02
49	PRIOR APPLICATION NUMBER: 60/103258
50	PRIOR FILING DATE: 1998-10-06
51	PRIOR APPLICATION NUMBER: 60/103314
52	PRIOR FILING DATE: 1998-10-07
53	PRIOR APPLICATION NUMBER: 60/103315
54	PRIOR FILING DATE: 1998-10-07
55	PRIOR APPLICATION NUMBER: 60/103328
56	PRIOR FILING DATE: 1998-10-07
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62	PRIOR FILING DATE: 1998-10-07
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66	PRIOR FILING DATE: 1998-10-08
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68	PRIOR FILING DATE: 1998-10-08
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70	PRIOR FILING DATE: 1998-10-08
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73	PRIOR APPLICATION NUMBER: 60/104257

PRIOR FILING DATE: 1998-10-14
PRIOR APPLICATION NUMBER: 60/104987
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/105000
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PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 60/105693
PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105694
PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105807

Query Match 100.0%; Score 1258; DB 11; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.4e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGEFCKPHSQPWOALFEKTRLLCGATLLIAPRWLLTAHCLKPRYIVHLGQHNLOKXE 60
DB 22 IIKGEFCKPHSQPWOALFEKTRLLCGATLLIAPRWLLTAHCLKPRYIVHLGQHNLOKXE 81
QY 61 GGEQRTTATESFPHGPNNSLPNKDRNDIMLVKASPVISITWAVRPLTSSRCVTAGTS 120
DB 82 GGEQRTTATESFPHGPNNSLPNKDRNDIMLVKASPVISITWAVRPLTSSRCVTAGTS 141
QY 121 CLISGSGTSSPOLRPLPHTLRCAANTIIIEHOKCENAYPGNITDTWVCASVOEGKDCSCOG 180
DB 142 CLISGSGTSSPOLRPLPHTLRCAANTIIIEHOKCENAYPGNITDTWVCASVOEGKDCSCOG 201
QY 181 DSGGPLVNCQSLQGIISWGQDPCAITRKPGVYTKVKCYVDWIOETMKN 229
DB 202 DSGGPLVNCQSLQGIISWGQDPCAITRKPGVYTKVKCYVDWIOETMKN 250

RESULT 2

US-10-015-387A-170
Sequence 170, Application US/10015387A
Publication No. US20030135034A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan I.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Pao, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2830PIC54
CURRENT APPLICATION NUMBER: US/10/015,387A
CURRENT FILING DATE: 2001-12-12
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 170
LENGTH: 250
TYPE: PRT
ORGANISM: Homo sapiens
US-10-015-387A-170

Query Match

100.0%; Score 1258; DB 12; Length 250;

Best Local Similarity 100.0%; Pred. No. 1.4e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGEFCKPHSQPWOALFEKTRLLCGATLLIAPRWLLTAHCLKPRYIVHLGQHNLOKXE 60
DB 22 IIKGEFCKPHSQPWOALFEKTRLLCGATLLIAPRWLLTAHCLKPRYIVHLGQHNLOKXE 81
QY 61 GGEQRTTATESFPHGPNNSLPNKDRNDIMLVKASPVISITWAVRPLTSSRCVTAGTS 120
DB 82 GGEQRTTATESFPHGPNNSLPNKDRNDIMLVKASPVISITWAVRPLTSSRCVTAGTS 141
QY 121 CLISGSGTSSPOLRPLPHTLRCAANTIIIEHOKCENAYPGNITDTWVCASVOEGKDCSCOG 180
DB 142 CLISGSGTSSPOLRPLPHTLRCAANTIIIEHOKCENAYPGNITDTWVCASVOEGKDCSCOG 201
QY 181 DSGGPLVNCQSLQGIISWGQDPCAITRKPGVYTKVKCYVDWIOETMKN 229
DB 202 DSGGPLVNCQSLQGIISWGQDPCAITRKPGVYTKVKCYVDWIOETMKN 250

RESULT 3

US-10-137-870-506
Sequence 506, Application US/10137870
Publication No. US20030138883A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ACIDS ENCODING THE SAME
FILE REFERENCE: P3330RIC155
CURRENT APPLICATION NUMBER: US/10/137,870
CURRENT FILING DATE: 2002-05-03
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 506
LENGTH: 250
TYPE: PRT
ORGANISM: Homo Sapien
US-10-137-870-506

Query Match 100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.4e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGEFCKPHSQPWOALFEKTRLLCGATLLIAPRWLLTAHCLKPRYIVHLGQHNLOKXE 60
DB 22 IIKGEFCKPHSQPWOALFEKTRLLCGATLLIAPRWLLTAHCLKPRYIVHLGQHNLOKXE 81
QY 61 GGEQRTTATESFPHGPNNSLPNKDRNDIMLVKASPVISITWAVRPLTSSRCVTAGTS 120
DB 82 GGEQRTTATESFPHGPNNSLPNKDRNDIMLVKASPVISITWAVRPLTSSRCVTAGTS 141
QY 121 CLISGSGTSSPOLRPLPHTLRCAANTIIIEHOKCENAYPGNITDTWVCASVOEGKDCSCOG 180
DB 142 CLISGSGTSSPOLRPLPHTLRCAANTIIIEHOKCENAYPGNITDTWVCASVOEGKDCSCOG 201
QY 181 DSGGPLVNCQSLQGIISWGQDPCAITRKPGVYTKVKCYVDWIOETMKN 229
DB 202 DSGGPLVNCQSLQGIISWGQDPCAITRKPGVYTKVKCYVDWIOETMKN 250

Query Match

100.0%; Score 1258; DB 12; Length 250;

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Db      202 DSGGPLVNCNOSLQGIISWGDPCCATITRKRGVYTKVCKYVDWIOETMKN 250

RESULT 4
US-10-140-018-506
; Sequence 506, Application US/10140018
; Publication No. US20030138885A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C158
; CURRENT APPLICATION NUMBER: US/10/140,018
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-018-506

Query Match      100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.4e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 IIKGECKPHSQPMQALFEKTRLLCGATLTAPRWLTAAHCLKRRIYVHIGQHNLOKEE 60
Db      22 IIKGECKPHSQPMQALFEKTRLLCGATLTAPRWLTAAHCLKRRIYVHIGQHNLOKEE 81
QY      61 GCEQRTATSEFPHPGFNNSLPNKDHRNDIMLVKASPVSTWAVRPLTSSRCVTAGTS 120
Db      82 GCEQRTATSEFPHPGFNNSLPNKDHRNDIMLVKASPVSTWAVRPLTSSRCVTAGTS 141
QY      121 CLISWGSTSSPOLRLPHTLRCAITITIEHOKCENAYPGNITDTMVCASVOEGKDCSCQG 180
Db      142 CLISWGSTSSPOLRLPHTLRCAITITIEHOKCENAYPGNITDTMVCASVOEGKDCSCQG 201
QY      181 DSGGPLVNCNOSLQGIISWGDPCCATITRKRGVYTKVCKYVDWIOETMKN 229
Db      202 DSGGPLVNCNOSLQGIISWGDPCCATITRKRGVYTKVCKYVDWIOETMKN 250

RESULT 5
US-10-140-021-506
; Sequence 506, Application US/10140021
; Publication No. US20030138886A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C167
; CURRENT APPLICATION NUMBER: US/10/140,021
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-021-506

Query Match      100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.4e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 IIKGECKPHSQPMQALFEKTRLLCGATLTAPRWLTAAHCLKRRIYVHIGQHNLOKEE 60
Db      22 IIKGECKPHSQPMQALFEKTRLLCGATLTAPRWLTAAHCLKRRIYVHIGQHNLOKEE 81
QY      61 GCEQRTATSEFPHPGFNNSLPNKDHRNDIMLVKASPVSTWAVRPLTSSRCVTAGTS 120
Db      82 GCEQRTATSEFPHPGFNNSLPNKDHRNDIMLVKASPVSTWAVRPLTSSRCVTAGTS 141
QY      121 CLISWGSTSSPOLRLPHTLRCAITITIEHOKCENAYPGNITDTMVCASVOEGKDCSCQG 180
Db      142 CLISWGSTSSPOLRLPHTLRCAITITIEHOKCENAYPGNITDTMVCASVOEGKDCSCQG 201
QY      181 DSGGPLVNCNOSLQGIISWGDPCCATITRKRGVYTKVCKYVDWIOETMKN 229
Db      202 DSGGPLVNCNOSLQGIISWGDPCCATITRKRGVYTKVCKYVDWIOETMKN 250

RESULT 6
US-10-140-274-506
; Sequence 506, Application US/10140274
; Publication No. US20030143674A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C161
; CURRENT APPLICATION NUMBER: US/10/140,274
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-274-506

Query Match          100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.4e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFECRPHSQWQALFEKTRLLCGATLIAPRWLITAAHCLKPRYIVHIGQHNLOKKE 60
DB 22 IIKGFECRPHSQWQALFEKTRLLCGATLIAPRWLITAAHCLKPRYIVHIGQHNLOKKE 81
QY 61 GCEQRTATSEFPHPGFNNSLPNKDRNDIMLVKMASPVSIWAVRPLTSSRCVTAGTS 120
DB 82 GCEQRTATSEFPHPGFNNSLPNKDRNDIMLVKMASPVSIWAVRPLTSSRCVTAGTS 141
QY 121 CLISGWGSTSSPOLRLPHTLRCAINTTIEHOKCENAYPGNITDTWVCASVQEGKDCSCG 180
DB 142 CLISGWGSTSSPOLRLPHTLRCAINTTIEHOKCENAYPGNITDTWVCASVQEGKDCSCG 201
QY 181 DSGGPLVNCNOSLOGIISWGODPCAITRRKPGVYTKVKCYVDWIQETMKN 229
DB 202 DSGGPLVNCNOSLOGIISWGODPCAITRRKPGVYTKVKCYVDWIQETMKN 250

RESULT 7
US-10-140-471-506
; Sequence 506, Application US/10140471
; Publication No. US2003013887A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddard, Paul J.
; APPLICANT: Goddard, Steven
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C163
; CURRENT APPLICATION NUMBER: US/10/140,471
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-471-506

Query Match          100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.4e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFECRPHSQWQALFEKTRLLCGATLIAPRWLITAAHCLKPRYIVHIGQHNLOKKE 60
DB 22 IIKGFECRPHSQWQALFEKTRLLCGATLIAPRWLITAAHCLKPRYIVHIGQHNLOKKE 81
QY 61 GCEQRTATSEFPHPGFNNSLPNKDRNDIMLVKMASPVSIWAVRPLTSSRCVTAGTS 120
DB 82 GCEQRTATSEFPHPGFNNSLPNKDRNDIMLVKMASPVSIWAVRPLTSSRCVTAGTS 141
QY 121 CLISGWGSTSSPOLRLPHTLRCAINTTIEHOKCENAYPGNITDTWVCASVQEGKDCSCG 180
```

```
DB 142 CLISGWGSTSSPOLRLPHTLRCAINTTIEHOKCENAYPGNITDTWVCASVQEGKDCSCG 201
QY 181 DSGGPLVNCNOSLOGIISWGODPCAITRRKPGVYTKVKCYVDWIQETMKN 229
DB 202 DSGGPLVNCNOSLOGIISWGODPCAITRRKPGVYTKVKCYVDWIQETMKN 250

RESULT 8
US-10-140-807-506
; Sequence 506, Application US/10140807
; Publication No. US2003013435A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddard, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C174
; CURRENT APPLICATION NUMBER: US/10/140,807
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-807-506

Query Match          100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.4e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKGFECRPHSQWQALFEKTRLLCGATLIAPRWLITAAHCLKPRYIVHIGQHNLOKKE 60
DB 22 IIKGFECRPHSQWQALFEKTRLLCGATLIAPRWLITAAHCLKPRYIVHIGQHNLOKKE 81
QY 61 GCEQRTATSEFPHPGFNNSLPNKDRNDIMLVKMASPVSIWAVRPLTSSRCVTAGTS 120
DB 82 GCEQRTATSEFPHPGFNNSLPNKDRNDIMLVKMASPVSIWAVRPLTSSRCVTAGTS 141
QY 121 CLISGWGSTSSPOLRLPHTLRCAINTTIEHOKCENAYPGNITDTWVCASVQEGKDCSCG 180
DB 142 CLISGWGSTSSPOLRLPHTLRCAINTTIEHOKCENAYPGNITDTWVCASVQEGKDCSCG 201
QY 181 DSGGPLVNCNOSLOGIISWGODPCAITRRKPGVYTKVKCYVDWIQETMKN 229
DB 202 DSGGPLVNCNOSLOGIISWGODPCAITRRKPGVYTKVKCYVDWIQETMKN 250

RESULT 9
US-10-140-922-506
; Sequence 506, Application US/10140922
; Publication No. US2003013889A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
US-10-140-922-506
```

```

; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C179
; CURRENT APPLICATION NUMBER: US/10/140,922
; PRIORITY FILING DATE: 2002-05-07
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-922-506

Query Match      100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.4e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IIKGECKPHSQPQOALFEKTRLLCGATLAPRWLLTAACHLKPRYIVHIGQHNLOKEE 60
DB 22 IIKGECKPHSQPQOALFEKTRLLCGATLAPRWLLTAACHLKPRYIVHIGQHNLOKEE 81
OY 61 GCEOTRTATESFPHGFNNSLPNKDHNDIMLVKASPVSTITWAVRPLTSSRCVTAGTS 120
DB 82 GCEOTRTATESFPHGFNNSLPNKDHNDIMLVKASPVSTITWAVRPLTSSRCVTAGTS 141
OY 121 CLISGSGTSSPOLRLPHTLRCAANTITIEHOKCENAVPGNITDTMVCAVVEGKDSGCG 180
DB 142 CLISGSGTSSPOLRLPHTLRCAANTITIEHOKCENAVPGNITDTMVCAVVEGKDSGCG 201
OY 181 DSGGPLVNCOSLQGIISWGDPCCATITRKPGVYTKVCKYVDMIOETMKN 229
DB 202 DSGGPLVNCOSLQGIISWGDPCCATITRKPGVYTKVCKYVDMIOETMKN 250

RESULT 10
US-10-140-924-506
; Sequence 506, Application US/10140924
; Publication No. US20030134355A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C177
; CURRENT APPLICATION NUMBER: US/10/140,924
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; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-924-506

Query Match      100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.4e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IIKGECKPHSQPQOALFEKTRLLCGATLAPRWLLTAACHLKPRYIVHIGQHNLOKEE 60
DB 22 IIKGECKPHSQPQOALFEKTRLLCGATLAPRWLLTAACHLKPRYIVHIGQHNLOKEE 81
OY 61 GCEOTRTATESFPHGFNNSLPNKDHNDIMLVKASPVSTITWAVRPLTSSRCVTAGTS 120
DB 82 GCEOTRTATESFPHGFNNSLPNKDHNDIMLVKASPVSTITWAVRPLTSSRCVTAGTS 141
OY 121 CLISGSGTSSPOLRLPHTLRCAANTITIEHOKCENAVPGNITDTMVCAVVEGKDSGCG 180
DB 142 CLISGSGTSSPOLRLPHTLRCAANTITIEHOKCENAVPGNITDTMVCAVVEGKDSGCG 201
OY 181 DSGGPLVNCOSLQGIISWGDPCCATITRKPGVYTKVCKYVDMIOETMKN 229
DB 202 DSGGPLVNCOSLQGIISWGDPCCATITRKPGVYTKVCKYVDMIOETMKN 250

RESULT 11
US-10-140-926-506
; Sequence 506, Application US/10140926
; Publication No. US20030134356A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C187
; CURRENT APPLICATION NUMBER: US/10/140,926
; PRIORITY FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 506
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-926-506

Query Match      100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.4e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IIKGECKPHSQPQOALFEKTRLLCGATLAPRWLLTAACHLKPRYIVHIGQHNLOKEE 60
DB 22 IIKGECKPHSQPQOALFEKTRLLCGATLAPRWLLTAACHLKPRYIVHIGQHNLOKEE 81
```

```

: GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Defoige, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zhen
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C208
CURRENT FILING DATE: 2002-05-08
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 506
LENGTH: 250
TYPE: PRT
ORGANISM: Homo Sapien
US-10-141-702-506

Query Match      100.0%; Score 1256; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1,4e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  IIKFECKPHSQPQQAALFEKTRLLCGATLIIAPRWLLTAAHCLKPRYIVHGHONLQKE 60
      |||
DB      22  IIKFECKPHSQPQQAALFEKTRLLCGATLIIAPRWLLTAAHCLKPRYIVHGHONLQKE 81

QY      61  GCEOTRATSFPIPGFNNSLPNKDHRNDIMLVKASPVSTIWMVRLPTLSSRCVTAGTS 120
      |||
DB      82  GCEOTRATSFPIPGFNNSLPNKDHRNDIMLVKASPVSTIWMVRLPTLSSRCVTAGTS 141

QY      121 CLISGWSSTSPQRLPHTRCANITIIHQKCNENAPGNITDTMVCASVOEGGKDSGOG 180
      |||
DB      142 CLISGWSSTSPQRLPHTRCANITIIHQKCNENAPGNITDTMVCASVOEGGKDSGOG 201

QY      181 DSGGFLVGNOSLGGIISWGODPCAITRKPGVYTKVKCYVDMIQETMKQN 229
      |||
DB      202 DSGGFLVGNOSLGGIISWGODPCAITRKPGVYTKVKCYVDMIQETMKQN 250

RESULT 14
US-10-141-704-506
: Sequence 506, Application US/10141704
: Publication No. US20030134359A1
: GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Defoige, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William

```

APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C209
CURRENT APPLICATION NUMBER: US/10/141,704
CURRENT FILING DATE: 2002-05-08
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 506
LENGTH: 250
TYPE: PRT
ORGANISM: Homo Sapien
US-10-141-704-506

Query Match 100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.4e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKFECKPHSQPWAALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHLGQHNLOKEE 60
DB 22 IIKFECKPHSQPWAALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHLGQHNLOKEE 81
QY 61 GCEQRTTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSTWAVRPLTLSSRCVTAGTS 120
DB 82 GCEQRTTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSTWAVRPLTLSSRCVTAGTS 141
QY 121 CLISGWGSTSSPOLRLPHTLRCAANTIIIEHOKCENAYPGNITDTMVCAVQEGGKDSGCG 180
DB 142 CLISGWGSTSSPOLRLPHTLRCAANTIIIEHOKCENAYPGNITDTMVCAVQEGGKDSGCG 201
QY 181 DSGGPLVNCQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKN 229
DB 202 DSGGPLVNCQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKN 250

RESULT 15

US-10-142-421-506
Sequence 506, Application US/10142421
Publication No. US20030134360A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C218
CURRENT APPLICATION NUMBER: US/10/142,421
CURRENT FILING DATE: 2002-05-09
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 506
LENGTH: 250
TYPE: PRT
ORGANISM: Homo Sapien
US-10-142-421-506

Query Match 100.0%; Score 1258; DB 12; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.4e-118;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIKFECKPHSQPWAALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHLGQHNLOKEE 60
DB 22 IIKFECKPHSQPWAALFEKTRLLCGATLLAPRWLLTAHCLKPRYIVHLGQHNLOKEE 81
QY 61 GCEQRTTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSTWAVRPLTLSSRCVTAGTS 120
DB 82 GCEQRTTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSTWAVRPLTLSSRCVTAGTS 141
QY 121 CLISGWGSTSSPOLRLPHTLRCAANTIIIEHOKCENAYPGNITDTMVCAVQEGGKDSGCG 180
DB 142 CLISGWGSTSSPOLRLPHTLRCAANTIIIEHOKCENAYPGNITDTMVCAVQEGGKDSGCG 201
QY 181 DSGGPLVNCQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKN 229
DB 202 DSGGPLVNCQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKN 250

Search completed: October 22, 2003, 15:54:44
Job time : 22.9589 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 23, 2003, 14:08:00 ; Search time 3410.8 seconds
(without alignments)
2746.659 Million cell updates/sec

Title: US-09-856-320A-2_COPY_54_282
Perfect score: 1258
Sequence: 1 IIRGFECKRHSQPMQALPE.....GYTVKVCXVVDIMQETMKNN 229

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2888711 segs, 20454813386 residues
Total number of hits satisfying chosen parameters: 5777422

Minimum DB seg length: 0
Maximum DB seg length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame+g2n.model -DEV=xih
-O=/cgn2.1/USPTO.spool/US09856320/runat_22102003.121414_25661/app_query.fasta_1.846
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=45
-UNITS=bits -START=1 -END=1 -MATRIX=blomsu62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=Pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=PCO -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09856320 @CGN_1_1_4326@runat_22102003.121414_25661 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -BSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl.*
1: gb_da.*
2: gb_hcg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*

29: em_vl.*
30: em_hcg_hum.*
31: em_hcg_inv.*
32: em_hcg_other.*
33: em_hcg_mus.*
34: em_hcg_pin.*
35: em_hcg_rtd.*
36: em_hcg_mam.*
37: em_hcg_vrt.*
38: em_sy.*
39: em_hcg_hum.*
40: em_hcg_mus.*
41: em_hcg_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1258	100.0	1106	6	AX016287 Sequence
2	1258	100.0	1106	6	BD137019 Human CAS
3	1258	100.0	1158	6	AX016289 Sequence
4	1258	100.0	1158	6	BD137020 Human CAS
5	1258	100.0	1181	6	AB013730 Homo sapi
6	1258	100.0	1186	9	AB012917 Homo sapi
7	1258	100.0	1192	6	AR152174 Sequence
8	1258	100.0	1204	6	AX358932 Sequence
9	1258	100.0	1204	6	AX362425 Sequence
10	1258	100.0	1204	6	AX454622 Sequence
11	1258	100.0	1204	6	AX464372 Sequence
12	1258	100.0	1204	6	AX491100 Sequence
13	1258	100.0	1204	6	AX491101 Sequence
14	1258	100.0	1213	6	BC022068 Homo sapi
15	1258	100.0	1301	6	BD091587 Novel ser
16	1258	100.0	1301	6	AB041036 Homo sapi
17	1258	100.0	1314	6	AR098430 Sequence
18	1258	100.0	1314	6	BD130920 Serine pr
19	1266	99.0	1166	6	AR152173 Sequence
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32	956	76.0	230000	9	AF243527 Homo sapi
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34	916.5	72.9	618	6	AC073185 Homo sapi
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37	885.5	70.4	176647	2	AC130782 Sequence
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40	782.5	62.2	243655	2	AC099172 Rattus no
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ALIGNMENTS

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 DEFINITION Sequence 1 from Patent WO949055.
 ACCESSION AX016287
 VERSION AX016287.1 GI:10041854
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 Bruck,C.E., Coche,T., Cassart,J.P. and Vinals-Bassols,C.
 Human casb12 polypeptide, a serine protease
 Patent: WO 949055-A 1 30-SEP-1999;
 BRUCK CLAUDE ELVIRE MARIE (BE); SMITHKLINE BEECHAM BIOLOG (BE);
 COCHE THIERRY (BE); CASSART JEAN POL (BE); VINALS BASSOLS CARLOTA
 (BE)

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BASE COUNT 247 a 348 c 287 g 224 t

ORIGIN

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US-09-856-320A-2_COPY_54_282 (1-229) x AX016287 (1-1106)

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 DB 233 AAGACGGCGCTACTCTGTGGGGCGAGCGCTCATCGCCCGAGATGGCTCTGACACAGCC 292

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QY 61 glycysgluglnthrtargthralathrgluserpheprohisprorglpheasnnsr 80
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QY 81 leuproasnlyasphisaargasnaspilmetleuvalysmetalaaserprovalser 100
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QY 121 cysleuilesergltytrpglyserthrserserproglngleuargleuprohisthrleu 140
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QY 221 TrpIleGlnIleuThrMetLysAsn 229
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 ACCESSION BD137019
 VERSION BD137019.1 GI:23231964
 KEYWORDS JP 2002507425-A/1.
 SOURCE Homo sapiens (human)
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 (bases 1 to 1106)
 Bruck,C.E.M., Cassart,J.P., Coche,T. and Bassols,C.V.
 Human CASB 12 polypeptide, a serine protease
 Patent: JP 2002507425-A 1 12-MAR-2002;
 SMITHKLINE BEECHAM BIOLOGICALS SA

AUTHORS
 TITLE
 JOURNAL

COMMENT
 OS Homo sapiens (human)
 PN JP 2002507425-A/1
 PD 12-MAR-2002
 PF 17-MAR-1999 JP 2000538015
 PR 20-MAR-1998 GB 9806095.7
 PI CLAUDE ELVIRE MARIE BRUCK,JEAN POL CASSART, THIERRY COCHE, PI
 CARLOTA VINALS BASSOLS
 PC C12N15/09,A61K31/70,A61K38/00,A61P35/00,A61P37/02,C07K16/40,
 PC C12N15/15,
 PC C12N1/19,C12N1/21,C12N5/10,C12N9/64,C12P21/02,C12Q1/02,C12Q1/
 PC 68,G01N33/15,
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 FT source

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 DB 773 GATCCCTGTGCGATACACCGAAAGCCTGTGTCTACACGAAAGTCTGCAAAATATGTGGAC 832
 QY 221 TrpIleGlnGluThrMetLysAsnAsn 229
 DB 833 TGGATCCAGAGACGATGAAGAACAT 859

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 VERSION AX016289.1 GI:10041855
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
 1 Bruck,C.E., Coche,T., Caessart,J.P. and Vinals-Bassols,C.
 Human casb12 polypeptide, a serine protease
 Patent: WO 94/9055-A 3 10-SEP-1999.

AUTHORS
 TITLE BRUCK CLAUDINE ELVIRE MARIE (BE); SMITHKLINE BECHAM BIOLOG (BE);
 JOURNAL COCHE THIERRY (BE); CASSART JEAN POL (BE); VINALS BASSOLS CARLOTTA (BE)

FEATURES
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BASE COUNT 274 a 359 c 306 g 219 t

ORIGIN

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 Score: 1258.00 Matches: 229
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 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x AX016289 (1-1158)

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 DB 303 AAGACGGGCTACTCTGTGGGGCAGAGCTCATATCGCCCAAGATGGCTCTGACAGCAGCC 362
 QY 41 HisCysLeuLysProArgTrpIleValHisLeuGlyGlnHisAsnLeuGlnLysGlu 60
 DB 363 CACTGCTCAAGCCCGCTACATAGTTCACTGGGGACACACACTCCAGAAAGAGAGAG 422
 QY 61 GlyCyseGluGlnThrArgThrAlaIaThrGluSerPheProHisProGlyPheAsnAsnSer 80
 DB 423 GGCTGTGACAGACCGGAGACAGACTGATGCTCTTCCCCACCCGGCTTCACACAGC 482
 QY 81 LeuProAsnLysAspHisAspAsnAspIleMetLeuValLysMetAlaSerProValSer 100
 DB 483 CTCGCCAACAACACACCGCAATGATCATCTGTGTAAGATGGCATGCGCATCTCC 542
 QY 101 IleThrTrpAlaValArgProLeuThrLeuSerSerArgCysValThrIleGlyThrSer 120
 DB 543 ATACCTGGGCTGTGGAGACCCCTCACCTCTCTCACGCTGTCTACTGTGGACACAGC 602
 QY 121 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140
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 QY 141 ArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTyrProGlyAsn 160
 DB 663 CGATGGCCAAACATCACCATCATTTAGACACCAAGAGTGAAGACCCCTAACCCGGCAAC 722
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 DEFINITION Human CASB 12 polypeptide, a serine protease.
 ACCESSION BD137020
 VERSION BD137020.1 GI:223231965
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
 1 Bruck,C.E.M., Caessart,J.P., Coche,T. and Bassols,C.V.
 Human CASB 12 polypeptide, a serine protease
 Patent: JP 2002507425-A 2 12-MAR-2002;

AUTHORS
 TITLE SMITHKLINE BECHAM BIOLOGICALS SA
 JOURNAL

COMMENT
 OS Homo sapiens (human)
 PN JP 2002507425-A/2
 PD 12-MAR-2002
 PF 17-MAR-1999 JP 2000538015
 PR 20-MAR-1998 GB 9806095.7
 PI CLAUDINE ELVIRE MARIE BRUCK,JEAN POL CASSART,THIERRY COCHE, PI
 CARLOTTA VINALS BASSOLS
 PC C12N15/09,A61K31/70,A61K38/00,A61P35/00,A61P37/02,C07K16/40,
 C12N1/15,
 PC C12N1/19,C12N1/21,C12N5/10,C12N9/64,C12P21/02,C12Q1/02,C12Q1/

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PC 68.G01N33/15
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CC Human CASB 12 polypeptide, a serine protease. FH Key
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DB 363 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGCAGCACAACCTCCAGAAAGAGAG 422
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QY 81 LeuProAsnLysASPHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
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QY 101 11etHrTPAlaValAlaArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
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DB 783 GACTCCGGGGGCGCTCTGTGTGTGAACGCTCTTCAAGGCAATATCTCCGGGGCGAG 842
QY 201 AspProCysAla11etHrArgLysProGlyValTyrThrLysValCysLysTyrValAsp 220
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DB 903 TGGATCCAGGAGACGATGAAGAAAT 929

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DEFINITION Homo sapiens mRNA for Hippocastin, complete cds.
ACCESSION AB013730
VERSION AB013730.1 GI:6681453
KEYWORDS Hippocastin.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (sites)
REFERENCE
AUTHORS Mitsui,S., Yamada,T., Okui,A., Komimami,K., Uemura,H. and
Yamaguchi,N.
TITLE A novel isoform of a kallikrein-like protease, TUSP/hippocastin,
(JPRS520), is expressed in the human brain and prostate
Biochem. Biophys. Res. Commun. 272 (1), 205-211 (2000)
JOURNAL 20329229
PUBMED 10872828
REFERENCES
AUTHORS Yamaguchi,N. and Mitsui,S.
TITLE Direct Submission
Submitted (08-MAY-1998) Nozomi Yamaguchi, Kyoto Prefectural
University of Medicine, Res. Ins. Geriatrics; Kawarimachi Hirokoji,
Kyoto, Kyoto 602-8566, Japan (E-mail:nozomi@koto.kpu-m.ac.jp,
Tel:81-75-251-5848, Fax:81-75-251-5848)
FEATURES
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QY	161	ILethrAspThrMetLeuValCysAlaSerValGlnGlnGlyGlyLysAspSerCysGlnGly	180
Db	664	ATCACAGACACCATGATGTGTGCCAGCGCGAGGAAGGGGCGAAGACCTCCGCCAGGGT	723
QY	181	AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerThrProGlyGln	200
Db	724	GATCTCGGGGGGCCCTCTGTGTCTGTAAACAGTCTTTCAGAGGATATATCTCCCTGGGGCCAG	783
QY	201	AspProCysAlaIleIleThrArgLysProGlyValIlyrThrLysValCysLysIlyrValAsp	220
Db	784	GATCCGATGTGCATACACCGAAGCCTGATGTCCTACGAAAGTCTGCAAATATATGTGGAC	843
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Db		185	ATCATCAAGGGGTTTGAGTGCAGAAGCTCAGTCCAGCCCTGGCAGGACGCCCTGTTCGAG	244
Oy		21	LysThrArgleuleuCySGilyAlATHrleulleaIaProArgTrpleuLeuthralaia	40
Db		245	AAGAGCGGGCTACTCTGTGGGGCACCGCTCATCCGCCACAGTGGCTCTTGACAGAGCC	304
Oy		41	HiscysLeuLysProArgTyrlIeValHisleuglyGlnHisasmeLunglinysglugu	60
Db		305	CACGCGCTCAAGCCCCGCTACATAGTTCACTGGGGCACACMACCTCCAGAAAGAGAG	364
Oy		61	GlyCySgluginThraArgThrAlATHrGlusErPheProHisProGlyPheasnAsner	80
Db		365	GGCGTGAGCGACCGGACGACGACCTAGTCTTCCCCACCAGCCCGGCTTCAACAACAC	424
Oy		81	LeuproAsnLysASPHisArgAsnAspiIemelleuValLysMerAlSerProValSer	100
Db		425	CTCCCCAACAAAGACCACCGCAAGACATCATGCTGTGAAGATGGCATCCGCAAGTCTCC	484
Oy		101	IlethrTpAlaValArgProleuThruiseSerSerArgCyvalTHrAlagLYthSer	120
Db		485	ATCACCTGGGGGTGTGGCAGCCCTCACCTCTCTCTACCGCTGTGTCAGTGTGGACACAGC	544
Oy		121	CysleulleSerGlyTTPrglySerThSerSerProGlnLeuArgLeuProHisThrleu	140
Db		545	TGCTCTATTCTCGGCTGGGGGACGACGTCCAGCCCCCAGTTACGCTGCTCTACACCTTG	604
Oy		141	ArgCyAlaAsnIleThrIleIleGIuHIsGInLysCysGiuaSnAlATyrProGlyAsn	160
Db		605	CGAGCGCCCAACATCACCATTCATTGAGCAGCACCAAGTGTGAAGAGCCTTACCCCGGCAAC	664
Oy		161	IleThrAspThrMetValCysAlSerValGInguLyglyLysASPSeCYsGIngly	180
Db		665	ATCACAACACCAAGTGTGTGTGCCAGCGTGCAGAAAGGGGGCAAGAGCATCTCCGCCAGGGT	724
Oy		181	AspserGlyGlyProLeuValCysASNginSerLeuGInglyIleIleSerTrypGlyGIn	200
Db		725	GATCCCGGGGGCCCTCTGGGTCTGTACCAAGTCTCTTCAAGGCATTATCTCTGGGGCCAG	784
Oy		201	ASPProCyAlaIleIleThrArgLysProGlyValTYrThryLysValCysLysTYrValasp	220
Db		785	GATCCGCTGTCGATCACCCGAAACCTCGTGTTCTACAGAAAGTCTGCAATAATATGTGAC	844
Oy		221	TripleGInguThrMetLysASnAsn	229
Db		845	TGCAATCAGAGACGATGAAGAACAAAT	871
RESULT 7				
LOCUS	ARI52174			
DEFINITION	Sequence 8 from patent US 6232456.	1192 bp	DNA	linear
ACCESSION	ARI52174			PAT 08-AUG-2001
VERSION	ARI52174.1	GI:15118224		
KEYWORDS				
SOURCE	Unknown.			

ORGANISM	Unknown:
REFERENCE	Unclafified.
AUTHORS	1 (bases 1 to 1192)
TITLE	Cohen, M., Colpitts, T. L., Friedman, P. N., Granados, E., Klass, M. R., Russell, J. C., Stewart, K. D. and Stroupe, S. D.
JOURNAL	Severe protease reagents and methods useful for detecting and treating diseases of the prostate
FEATURES	Patent: US 6232456-A 8 15-MAY-2001;
source	Location/Qualifiers 1. 1192
BASE COUNT	279 a 385 c 290 g 238 t
ORIGIN	/organism="unknown"
Alignment Scores:	
Pred. No.:	4,48e-97 Length: 1192
Score:	1258.00 Matches: 229
Percent Similarity:	100.00% Conservative: 0
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Query Match:	100.00% Indels: 0
DB:	Gaps: 0
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QY	1 11e11eysglYpHeGlucYslySProHissERGInProTTPGlnAla1Ala1ePheGlu 20
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QY	21 lyethrArgleuencysglyAla1eThrLeu11eAlaProArgTTPLeuThlAla 40
Db	230 AAGAGCGGGTACTCTGTGGGGGAGAGCTATCGCCCCAGATGGCTCTTACAGCAGCC 289
QY	41 H1eCysleuYsPProArGTYr11eAla1H1sleuGlyGlnH1sAsn1eGln1sleuGlu 60
Db	290 CACGCGCTCAAGCCCGCCATCAAGTTCACCTGGGGCAGACACCTCCAGAAAGAGAG 349
QY	61 GlyCysGluGlnThrArgThralaThrGusPheProHissProGlyPheAsnAsnSer 80
Db	350 GGCTGTAGACAGCCCGGACAGCCATGTAGTCTTCCCAACCCCGCTTCAACAGAGC 409
QY	81 LeuProAsn1ysAspH1sArgAsnAsp11eMetLeuAla1ysMetAlaSerProValSer 100
Db	410 CTCCCCAACAAGAACACCGCAATGACATCAAGCTGTGAAGATGGCATCGCCAGTCTCC 469
QY	101 11eThrTrpAlaValArGPProLeuThrLeuSerSerArGysValThralaGlyThrSer 120
Db	470 ATACACCGGGCTGTGCAGACCCCTCACCTCTCTCACGCTGTGTACATCGTGGACAC 529
QY	121 CysLeu11eSerGlyTYrTPGlySerThrSerSerProGlnLeuArgLeuProHissThrLeu 140
Db	530 TGCCTCATTTTCGGGCTGGGGCAGACAGTCCACACCCCAAGTTACGCTTCCACACCTTG 589
QY	141 ArgCysAlaAsn11eThr11eGlnH1sGln1ysCysGlnAsnAla1TYrProGlyAsn 160
Db	590 CGAGCGCCCAACATCACCAATCATTTGACACCGAAGGTGAGAAAGCGCTTACCCGGCAAC 649
QY	161 11eThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGlnGly 180
Db	650 ATCAACAGACCACTGGTGTGTGTGCACCGTGCAGAAAGGGGCAAGAGATCTCTGCCAGGT 709
QY	181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGly11e11eSerTYrGlyGln 200
Db	710 GACTCCGGGGGCCCTCTGGTCTGTACAGTCTTTCAAGGATATATCTCTGGGGCAG 769
QY	201 AspProCysAla11eThrArgLysProGlyValTYrThrLysValCysLysTYrValAsp 220
Db	770 GATCCGGTGTCCGATCACCCGAAAGCGCTGTGTCTACAGAAAGTCTGCAGAAATATGTGAC 829
QY	221 Trp11eGlnGlnThrMetLysAsnAsn 229
Db	830 TGGATCCAGGAGACGATGAAGAACAAT 856

AX358932	AX358932	1204 bp	DNA	linear	PAT 13-FEB-2002
LOCUS	Sequence 185 from Patent WO0193983.				
DEFINITION	AX358932				
ACCESSION	AX358932				
VERSION	AX358932.1	GI:18675367			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A., Godoweki, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P., Watanabe, C.K. and Wood, W.I.				
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same				
JOURNAL	Patent: WO 0193983-A 185 13-DEC-2001;				
FEATURES	Genentech Inc. (US)				
source	Location/Qualifiers				
	1..1204				
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BASE COUNT	306 a 364 c 294 g 240 t				
ORIGIN					
Alignment Scores:					
Pred. No.:	4,53e-97	Length:	1204		
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Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	100.00%	Indels:	0		
DB:	6	Gaps:	0		
US-09-856-320A-2_COPY_54_282 (1-229) x AX358932 (1-1204)					
QY	1	11e11e1ygs1yphEg1uCyE1ySP1rohiSseG1nPr0Tg1n1a1a1a1eupheG1u	20		
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QY	21	1yS1hr1r1g1e1u1e1uCySg1yAl1a1Th1e1u1e1a1Pr0a1gT1rPl1e1u1e1Th1a1a1a	40		
DB	229	AAGACGGGGCTACTCTGTGGGGCCAGCCTCATCCCCCAAGATGCTCTGTACAGCAGCC	288		
QY	41	HiSc1yS1e1u1ySP1r0A1gT1y11e1v1a1h1S1e1u1g1y1n1h1S1a1e1u1G1n1yS1g1u1u	60		
DB	289	CAC1GCGCTCAAGCCCCCGTCATATGATGTTCACTGGGGCAGCAGCAACCTCCAGAGAGAG	348		
QY	61	G1yCySg1uG1n1h1r1a1gT1h1a1l1Th1G1uS1e1rPhe1Pro1h1SP1r0G1yPhe1A1n1S1e1r	80		
DB	349	GGGTGTGAGCAGACCCGGACAGCCACGTAGCTCTCCCCCACCCGGCTTCACACAGC	408		
QY	81	Leu1r0a1e1n1yS1a1rP1h1S1a1rG1a1n1A1rP11e1w1e1t1e1u1a11yS1e1t1a1S1e1rP1r0a1S1e1r	100		
DB	409	CTCCCCAACAAGACACCCGCAATGAAATATCATGTGGTGAAGATGGCATCCCAAGTCTCC	468		
QY	101	11e1h1r1r1a1a1a1A1rG1P1r01e1u1Th1e1uS1e1rS1e1r1h1G1yS1a1V1a11h1r1a1a1g1yTh1S1e1r	120		
DB	469	ATCACCTGGGGCTGTGGCAACCCCTCAACCTCTCTCTACAGCTGTGTCACTGCTGGACACAGC	528		
QY	121	CyS1e1u1e1S1e1rG1yT1rP1g1yS1e1rTh1S1e1rS1e1rP1r0G1n1e1u1a1rG1e1u1P1r0h1S1Th1e1u	140		
DB	529	TGCTCATATTCGGGCTGGGGCAGCAGCGTCCAGCCCCAGTTAAGCTTCCTACACCTTTG	588		
QY	141	ArG1CyS1a1a1a1n11e1h1r11e11e1G1n1h1S1g1n1yCySg1u1a1n1a1A1T1y1rP1r0G1y1a1n	160		
DB	589	CGAATGGCCCAACATCACCATCATATGACACACAGAGTGTGAAACGGCTTACCCCGGCAAC	648		
QY	161	11e1h1r1a1rP1h1e1t1a1CyS1a1a1S1e1V1a1G1n1u1n1g1y1g1y1yS1a1S1e1rCySg1n1g1y	180		
DB	649	ATCACAGACACCAATGATGTGTGTCCAGGCTGACGAGAAAGGGGACAGACTCTCCGACAGGT	708		
QY	181	ASp1e1rG1yG1yP1r01e1u1a1CyS1a1nG1n1S1e1r1e1u1n1g1y11e11e1S1e1rT1rP1g1yG1n	200		

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Db 709 GACTCCGGGGCCCTGCTCTGTAACCACTCTCTCAAGCATTTATCTCTGGGGCAG 768
QY 201 AASPProCysAlaIleThrArglyProGlyValTYrThrlYsValCyslyTyValAsp 220
Db 769 GATCCGTGTGGCATCACCCGAAAGCCGTGTCTACAGAAAGTTCGAAATATGTGGAC 828
QY 221 TTPILGInGUThrMetLysAsnAsn 229
Db 829 TGGATCCAGAGACGATGAAGAACAT 855
RESULT 9
AX362425 1204 bp DNA linear PAT 15-FEB-2002
LOCUS Sequence 185 from Patent WO0208288.
DEFINITION AX362425
ACCESSION AX362425
VERSION AX362425.1 GI:18694670
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
Watanabe,C.K. and Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0208288-A 185 31-JAN-2002;
Genentech, Inc. (US)
FEATURES
source 1..1204
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 306 a 364 c 294 g 240 t
ORIGIN
Alignment Scores:
Pred. No.: 4.53e-97 Length: 1204
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
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Db 169 ATCATTAAGGGGTTGAGTGCAGAGCTTCACTCCAGCCCTGGCAGGACCCCTGTTCCAG 228
QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTyrLeuLeuThrlAla 40
Db 229 AAGAGCGGCTACTGTGTGGGGGAGCGCTCATCGCCGCCAGATGGCTTCGACAGAGC 288
QY 41 HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlu 60
Db 289 CACTGCTCTCAAGCCCGCTACATAGTTCACTGGGGCAGACACACCTCCAGAGAGGAG 348
QY 61 GlyCysGluGlnThrArgThrlAlaThrGlnSerPheProHisProGlyPheAsnAsnSer 80
Db 349 GGCTGTGAGCAGACCCGAGCAGCCACTGAGTCTTCCCGACCCGGCTTCAACACAGC 408
QY 81 LeuProAsnLysAspHisIleArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
Db 409 CTCGCCCAACAAAGACCAACGCAATGATCATGTGTGTAAGATGATGATGCGCAGCTCC 468
QY 101 IleThrTrrAlaValArgProLeuThrLysSerSerArgCysValThrlAlaGlyThrSer 120
Db 469 ATTCACCTGGGCTGTGGACCCCTCACTCTCTCAACGCTGTGTCACTGCTGGACACAGC 528
QY 121 CysLeuIleSerGlyTrrpLysThrSerSerProGlnLeuArgLeuProHisThrIleu 140

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Db 529 TGGCTATTTCGGGCTGGGGGAGCAGCTCCAGCCCACTTACGCTGCTCACACCTTG 588
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Db 589 CAGTGGCCCAACATCACCATCATTTGAGCACCAAGAGTGTGAGAACGCCATACCCGGCAAC 648
QY 161 IleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGlnGly 180
Db 649 ATTCACAGACACCATGCTGTGTCCACGTCGAGGAAGGGGGAGAGACTCTCCAGGGGT 708
QY 181 AASPserGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrrpGlyGln 200
Db 709 GACTCCGGGGGCCCTCTGCTGTGTAACCACTCTCTCAAGCATTTATCTCTGGGGCAG 768
QY 201 AASPProCysAlaIleThrArglyProGlyValTYrThrlYsValCyslyTyValAsp 220
Db 769 GATCCGTGTGGCATCACCCGAAAGCCGTGTCTACAGAAAGTTCGAAATATGTGGAC 828
QY 221 TTPILGInGUThrMetLysAsnAsn 229
Db 829 TGGATCCAGAGACGATGAAGAACAT 855
RESULT 10
AX454622 1204 bp DNA linear PAT 06-JUL-2002
LOCUS Sequence 207 from Patent WO0208284.
DEFINITION AX454622
ACCESSION AX454622
VERSION AX454622.1 GI:21713935
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.I.,
Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
and Ye,W.
TITLE Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
JOURNAL Patent: WO 0208284-A 207 31-JAN-2002;
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone
(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)
; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William
I. (US)
FEATURES
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/db_xref="taxon:9606"
BASE COUNT 306 a 364 c 294 g 240 t
ORIGIN
Alignment Scores:
Pred. No.: 4.53e-97 Length: 1204
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-09-856-320a-2_COPY_54_282 (1-229) x AX454622 (1-1204)
QY 1 IleIleLysGlyPheGluCysLysProHisSerGlnProTTPGlnAlaIleuPheGlu 20
Db 169 ATCATTAAGGGGTTGAGTGCAGAGCTTCACTCCAGCCCTGGCAGGACCCCTGTTCCAG 228
QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTyrLeuLeuThrlAla 40

```

Db      229 AAGAGCGGCTACTCTGTGGGCGAGCTCATCGCCCGCAAGTGGCTCTGTACAGAGCC 288
QY      41 HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlu 60
Db      289 CACTGGCTCAAGCCCCCGCTACATAGTTTACCTGGGGCAGACACACTCCAGAAAGGAGG 348
QY      61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80
Db      349 GGCTGTGACAGACCCGAGCAGCCACTGAGTCTTCCCGCCACCCCGGCTTCAACACAGC 408
QY      81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
Db      409 CTCCTCCCAACAAAGACCCGCAATGACATCATGCTGGTGAAGATGGCATCGCAGTCTCC 468
QY      101 ILeuThrPalValAlaArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
Db      469 ATCAGCTGGGCTGTGGACCCCTCAGCCCTCTCTCAGCTGTGTCTGCTGACAGCAGC 528
QY      121 CysLeuLysSerGlyTyrGlySerThrSerSerProGlnLeuValGluLeuProHisThrLeu 140
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QY      141 ArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTyrProGlyAsn 160
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QY      161 ILeuThrPalValAlaArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 180
Db      649 ATCAGACAGACACCATGGTGTGTGCCAGCGTGCAGAAAGGGGCGCAAGACTCTGCCAGGT 708
QY      181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTyrGlyGln 200
Db      709 GACTCGGGGGGCGCTCTGTGTGTGAACAGTCTCTTCAAGGCAATATCTCCGGGGCCAG 768
QY      201 AspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrValAsp 220
Db      769 GATCGCTGTGCATCACCGGAAGCTGTGTCTACAGAAAGTCTGCMAATATGTGGAC 828
QY      221 TTPileGlnGluThrMetLysAsnAsn 229
Db      829 TGGATCCAGAGACGATGAAGAACAAT 855

RESULT 11
AX464372 1204 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 505 from Patent WO0140466.
ACCESSION AX464372
VERSION AX464372.1 GI:21899202
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
1 Baker K.P., Beresini M., DeForge L., Desnoyers L., Filvaroff E.,
Geo W.Q., Gerritsen M.E., Goddard A., Godowski P.J., Gurney A.L.,
Sherwood S., Smith V., Stewart T.A., Tunas D., Watanabe C.K.,
Wood W.L. and Zhang Z.
Secreted and transmembrane polypeptides and nucleic acids encoding
same
JOURNAL Patent: WO 0140466-A 505 07-JUN-2001;
Genentech Inc. (US)
FEATURES
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 306 a 364 c 294 g 240 t
ORIGIN
Alignment Scores: 4.53e-97 Length: 1204
Pred. No.: 1258.00 Matches: 229
Score: " "

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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

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Db      229 AAGAGCGGCTACTCTGTGGGCGAGCTCATCGCCCGCAAGTGGCTCTGTACAGAGCC 288
QY      41 HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGluGlu 60
Db      289 CACTGGCTCAAGCCCCCGCTACATAGTTTACCTGGGGCAGACACACTCCAGAAAGGAGG 348
QY      61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80
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QY      101 ILeuThrPalValAlaArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
Db      469 ATCAGCTGGGCTGTGGACCCCTCAGCCCTCTCTCAGCTGTGTCTGCTGACAGCAGC 528
QY      121 CysLeuLysSerGlyTyrGlySerThrSerSerProGlnLeuValGluLeuProHisThrLeu 140
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QY      141 ArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTyrProGlyAsn 160
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QY      161 ILeuThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGlnGly 180
Db      649 ATCAGACAGACACCATGGTGTGTGCCAGCGTGCAGAAAGGGGCGCAAGACTCTGCCAGGT 708
QY      181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTyrGlyGln 200
Db      709 GACTCGGGGGGCGCTCTGTGTGTGAACAGTCTCTTCAAGGCAATATCTCTGGGGCCAG 768
QY      201 AspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrValAsp 220
Db      769 GATCGCTGTGCATCACCGGAAGCTGTGTCTACAGAAAGTCTGCMAATATGTGGAC 828
QY      221 TTPileGlnGluThrMetLysAsnAsn 229
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RESULT 12
AX491100 1204 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 207 from Patent WO0200690.
ACCESSION AX491100
VERSION AX491100.1 GI:22323887
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
1 Baker K.P., Ferrara N., Gerber H., Gerritsen M.E., Goddard A.,
Godowski P.J., Gurney A.L., Hillan K.J., Marsters S.A., Pan J.,
Paoni N.F., Stephan J.P., Watanabe C.K., Williams P.M., Wood W.L.
and Ye W.
Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis

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JOURNAL Patent: WO 0200690-A 207 03-JAN-2002;
Genentech, Inc. (US)
Location/Qualifiers
FEATURES
source 1..1204
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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QY 41 HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGlnGlu 60
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Db 469 ATCACTGGGGCTGTGGACCCCTCCTCTCTCCACGCTGTGCTCACTGTGGCAGCAGC 528
QY 121 CysLeuIleSerGlyTyrGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140
Db 529 TGCCCTATTTCGGGCTGGGGGAGCAGCTCCAGCCCGCAGTTACGCTGCTCACACCTTG 588
QY 141 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTyrProGlyAsn 160
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LOCUS AX697101
DEFINITION Sequence 169 from Patent WO0078961.
ACCESSION AX697101

VERSION AX697101.1 GI:29498066
KEYWORDS
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ORGANISM Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
1 Ferrera, N., Stewart, T.A., Williams, P.M., Baker, K.P., Desnoyers, L.,
Eaton, D.L., Gao, W.Q., Pan, J., Botstein, D., Fong, S., Goddard, A.,
Godowski, P.J., Gunney, A.L., Smith, V., Tunas, D., Wood, W.I.,
Grimaldi, C.J., Hillan, K.J., Paoni, N.F., Roy, M.A. and Watanabe, C.K.
Secreted and transmembrane polypeptides and nucleic acids encoding
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JOURNAL Patent: WO 0078961-A 169 28-DEC-2000;
Genentech, Inc. (US)
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Best Local Similarity: 100.00% Mismatches: 0
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QY 41 HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGlnGlu 60
Db 289 CACTGCGCTCAAGCCCGGCTCATAGTTCACTCGGGGAGACACAACCTCCAGAGAGAGAG 348
QY 61 GlyCysGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsnSer 80
Db 349 GGGTGTGAGCAGACCCGGAGCAGCAGCTGAGTCTTCCCCACCCCGCTTCAACACAGC 408
QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
Db 409 CTCGCCAACAAAGACACCGGCATGATCATGCTGTGAGATGGCATGCCAGTCTCC 468
QY 101 lletthtrpalaalavargproleuthrleuenserargcysvalthrilaaglythrser 120
Db 469 ATCACTGGGGCTGTGGACCCCTCCTCTCTCCACGCTGTGCTCACTGTGGCAGCAGC 528
QY 121 CysLeuIleSerGlyTyrGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140
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QY 141 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTyrProGlyAsn 160
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QY 161 lletthaspthrmetvalcysalaservalglnuglyglylyaspsercysglngly 180
Db 649 ATCAACAGACACATGTGTGTGTCACAGCTGACAGAGGGGGCAAGAGTCTCTGGCAGGT 708
QY 181 AspSerGlyGlyProleuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200
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QY 201 AepProcysalalIethrArGlyProGlyValTyThrThyValCysLysTyValAsp 220
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 Db 829 TGGATCCAGAGACGATGAGAACAAAT 855

RESULT 14
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 DEFINITION complete cds.

ACCESSION BC022068
 VERSION BC022068.1 GI:18314497
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1213)
 AUTHORS Strausberg,R.
 TITLE Direct Submission
 JOURNAL Submitted (22-JAN-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: http://mgc.nci.nih.gov
 REMARK Contact: MGC help desk
 COMMENT Email: cgaabs-r@mail.nih.gov
 Tissue Procurement: Miklos Pal Kovits, M.D., Ph.D.
 CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Institute for Systems Biology
 http://www.systemsbio.org
 contact: amadan@systemsbio.org
 Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha
 Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

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BASE COUNT 290 a 376 c 296 g 251 t
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Alignment Scores:
 Pred. No.: 4.57e-97 Length: 1213
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us-09-856-320a-2_copy_54_282 (1-229) x BC022068 (1-1213)

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QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuLeaIaProArgTrrPLeuLeuThraIa 40
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 Db 256 AAGAGCGGCTACTCTGTGGGGCAGCTCATTCGCCCAATGCTCTTCAAGCAGACC 315

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 Db 316 CACTGCCTCAAGCCCGGCTACATAGTTCACCTGGGGCAGCAACCTCCAGAGAGAG 375

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QY 121 CysLeuLeuSerArgYrrPGLysThrSerSerProGlnLeuArgLeuProHisThrLeu 140
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 LOCUS Novel serine protease BSSP6.
 DEFINITION BD091587
 ACCESSION BD091587.1 GI:22637198
 VERSION BD091587.1
 KEYWORDS WO 0031257-A/1.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1301)
 AUTHORS Uemura,H., Okui,A., Kominami,K., Yamaguchi,N. and Mitsui,S.
 TITLE Novel serine protease BSSP6
 JOURNAL Patent: WO 0031257-A 1 02-JUN-2000;
 FUSO PHARMACEUTICAL INDUSTRIES LTD, HIDEOTOSHI UEMURA, AKIRA OKUI,
 KATSUYA KOMINAMI, NOZOMI YAMAGUCHI, SHINICHI MITSUI
 COMMENT OS Homo sapiens (human)
 PN WO 0031257-A/1

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GenCore version 5.1.6
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Run on: October 23, 2003, 14:05:42 ; Search time 251.855 Seconds
(without alignments)
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Listing first 45 summaries

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and is derived by analysis of the total score distribution.

SUMMARIES

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8	1258	100.0	1204	22	AAF54320
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16	1258	100.0	1301	21	AAA61763
17	1258	100.0	1314	21	AAZ30222
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19	1248	99.2	1146	22	ABA83430
20	1246	99.0	1166	22	AAD14841
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26	1213	96.4	833	19	AAV42925
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29	916.5	72.9	618	24	ABK30233
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32	736	58.5	1375	22	AAS26876
33	736	58.5	1438	24	ABQ99555
34	736	58.3	1365	22	AAS41087
35	716	56.9	924	22	AAS41622
36	716	56.9	924	22	AAS26948
37	716	56.9	924	23	ABK41855
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40	684	54.4	1333	18	AAT63251
41	683	54.3	942	20	AAT1030
42	682	54.2	963	24	AAD30570
43	682	54.2	963	24	ABK1774
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ALIGNMENTS

RESULT 1

AAZ22638

AAZ22638 standard; cDNA; 1106 BP.

AAZ22638;

08-DEC-1999 (first entry)

CASB12 nucleotide sequence.

neuropilin; cancer; assay; inhibitor; serine protease; immunogenic;

ds.

Homo sapiens.

Key Location/Qualifiers

CDS 14..862

Pred. No.: 4,95e-105 Length: 1186
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-09-856-320a-2_copy_54_282 (1-229) x ABX76468 (1-1186)

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DB 845 TGGATCCAGAGACGATGAAGAACAT 871

RESULT 4
ABX76468
ID ABX76468 standard; DNA; 1186 BP.

AC ABX76468;
DT 02-APR-2003 (first entry)

DE Lung cancer-associated polynucleotide #312.

KW Lung cancer-associated polynucleotide; gene; ds. cytoskeletal; emphysema;
antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

OS Unidentified.

PN WO200286443-A2.

XX 31-OCT-2002.

PF 18-APR-2002; 2002WO-US12476.

PR 18-APR-2001; 2001US-284770P.

PR 10-MAY-2001; 2001US-290492P.

PR 09-NOV-2001; 2001US-339245P.

PR 13-NOV-2001; 2001US-350666P.

PR 29-NOV-2001; 2001US-334370P.

PR 12-APR-2002; 2002US-372246P.

XX (EOSB-) EOS BIOTECHNOLOGY INC.

PI Aziz N. Murray R;

DR WPI: 2003-093161/08.

XX P-PSDB; ABU56739.

PT Detecting a lung cancer-associated transcript in a cell from a patient

PT for treating lung cancer, by contacting a biological sample from the

PT patient with a polynucleotide that exhibits increased or decreased

PT expression in lung cancer

PS Claim 22; Page 443; 453pp; English.

XX The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridises
CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung
CC cancer-associated polynucleotides and polypeptides are used for
CC identifying a compound that modulates a lung cancer-associated
CC polypeptide, for inhibiting proliferation of a lung cancer-associated
CC cell to treat lung cancer in a patient and for treating a mammal having
CC lung cancer by administering a modulatory compound identified. The
CC methods are useful for treating lung cancer, such as small cell lung
CC cancer, non-small cell lung cancer or other benign or precancerous
CC lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive
CC pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial
CC and polypeptides are useful for diagnostic purposes and as targets for
CC screening for therapeutic compounds that modulate lung cancer, such as
CC antibodies. Sequences ABX76124-ABX76474 represent lung cancer-associated
CC polynucleotides of the invention.

XX SQ Sequence 1186 BP; 272 A; 368 C; 302 G; 244 T; 0 other:

Alignment Scores:

Pred. No.: 4,95e-105 Length: 1186
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 25 Gaps: 0

US-09-856-320a-2_copy_54_282 (1-229) x ABX76468 (1-1186)

QY 1 llellelysglypnehlucylsyserprohisergerinprotrpinaalaleuphegu 20
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QY 21 LysThrArgLeuLeuCySGlYAlaThrLeuilealaproargTprleuLeuThraAla 40
DB 304 245 AAGACGGGCTACTGTGGGGGAGAGCTCATCGCCAGATGGCTCTGACAGCAGCC 304
QY 41 HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnLysGlnGu 60
DB 364 305 CACTGCTCAAGCCCGCTACATAGTTCACCTGGGGGAGAGCAACCTCCAGAAAGAGAG 364

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QY 61 GlyCysGluGlnThrArgThrAlaThrGlnGlnSerPheProHisProGlyPheAsnAsnSer 80
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QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
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QY 101 IleThrTPAlaValAlaArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
Db 485 ATCACTGGGCTGTGTGGACCCCTCACCCTCTCTCAAGCTGTGTCACTGTGGCACCAGC 544
QY 121 CysLeuIleSerGlyTyrGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140
Db 545 TGCTCATTTCCGGCTGGGGCAGCAGCTCCAGCCCAAGTACGCTTGCCTCAGCCTTG 604
QY 141 ArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTyrProGlyAsn 160
Db 605 CGATGCGCCAACTACCATCATGTAGACACAGAAAGTGTAGAACCCCTAACCCGGCAAC 664
QY 161 IleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGlnGly 180
Db 665 ATCAGACAGACCATGATGTGTGTCCAGCTGCAGAAAGGGGCAAGGACTCTGCGAGGT 724
QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTyrGlyGln 200
Db 725 GACTCGGGGGCCCTGTGTGTGTACAGCTCTTCAAGGCAATATCTCTGGGGCCAG 784
QY 201 AspProCysAlaIleThrArgLysProGlyValTyrThrLysValCysLysTyrValAsp 220
Db 785 GATCCGCTGTGCATCACCCGAAAGCTGTGTGTACAGAAAGTGTGAAATATGTGAC 844
QY 221 TrpIleGlnGluThrMetLysAsnAsn 229
Db 845 TGAATCAGAGACGATGTGTGAAAGCAAT 871
RESULT 5
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XX AADI4842;
AC AADI4842;
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XX 01-NOV-2001 (first entry)
XX
XX Human PS133 gene contig.
XX
XX Human; PS133; prostate disease; cancer; immunogen; gene therapy; EST;
XX expressed sequence tag; cytostatic; ds.
XX
XX Homo sapiens.
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XX Key Location/Qualifiers
XX CDS 107..859
XX /*tag= a
XX /product= "Human PS133 protein"
XX /transl_except= (pos:188..196, aa:Cys-Pro)
XX /transl_except= (pos:224..232, aa:Phe-Lys)
XX
XX US6232456-B1.
XX
XX 15-MAY-2001.
XX
XX 06-OCT-1997; 97US-0944483.
XX
XX 06-OCT-1997; 97US-0944483.
XX
XX (ABBO ) ABBOTT LAB.
XX
XX Cohen M, Colclitts TL, Friedman PN, Granados E, Klass MR;
XX Russell JC, Stewart KD, Stroupe SD;
XX WPI; 2001-366357/38.
XX
XX P-PSDB; AAE08017.
```

```
XX
XX New PS133 polynucleotides, useful for detecting, diagnosing, staging,
XX monitoring, prognosing, preventing, treating or determining the
XX predisposition of an individual to a prostate disease, e.g. cancer -
XX Claim 1, Column 71-74; 93pp; English.
XX
XX The patent discloses PS133 polynucleotides and polypeptides which
XX are indicative of prostate disease. The patent also provides a method
XX for detecting PS133 protein in a test sample. The polynucleotides of
XX the invention are useful for detecting, diagnosing, staging, monitoring,
XX prognosing, preventing, treating or determining the predisposition of
XX an individual to prostate diseases such as cancer. PS133-derived
XX polynucleotides are used for the detection of normal or altered gene
XX expression, in assays for detecting, amplifying or quantifying genes
XX or nucleic acids relating to prostate tissue diseases and conditions,
XX and to produce probes which can be used in the detection of nucleic
XX acids in a sample. PS133 proteins are used as immunogens for the
XX production of antibodies. PS133 sequences are also used in gene
XX therapy. The present sequence is human PS133 gene contig.
XX
XX Sequence 1192 BP; 279 A; 385 C; 290 G; 238 T; 0 other;
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Alignment Scores:

Pred. No.:	4,986-105	Length:	1192
Score:	1258.00	Matches:	229
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0

US-09-856-320A-2_COPY_54_282 (1-229) x AADI4842 (1-1192)

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QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTyrLeuLeuThrAlaAla 40
Db 230 AAGACGGCGCTACTGTGTGGGGGAGCGCTCATCGCCCGCCAGATGAGTCTCTGACAGAGCC 289
QY 41 HisCysLeuLysProArgTyrIleValHisLeuGlyGlnHisAsnLeuGlnGlyGln 60
Db 290 CACTGCTCTAAGCCCCCGCTACATAGTTCACTCGGGGACAGACAACTCTCAGAAAGAGAG 349
QY 61 GlyCysGluGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsnSer 80
Db 350 GGCTGTGAGACAGACCCGGACAGCCACTGAGTCTTCCGCCACCCGGCTTCAACAACAGC 409
QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
Db 410 CTCGCCAACAAACACACCGCAATGACATCATGCTGTGAAATGTCATGCGCAGTCTCC 469
QY 101 IleThrTPAlaValAlaArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
Db 470 ATCACTGGGCTGTGTGGACCCCTCACCCTCTCTCAAGCTGTGTCACTGTGGCACCAGC 529
QY 121 CysLeuIleSerGlyTyrGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140
Db 530 TGCTCATTTCCGGCTGGGGCAGCAGTCCAGCCCGCAAGTACGCTGCTCAGCCTTG 589
QY 141 ArgCysAlaAsnIleThrIleIleGluHisGlnLysCysGluAsnAlaTyrProGlyAsn 160
Db 590 CGATGCGCCAACTACCATCATGTAGACACAGAAAGTGTAGAAAGCCCTAACCCGGCAAC 649
QY 161 IleThrAspThrMetValCysAlaSerValGlnGluGlyLysAspSerCysGlnGly 180
Db 650 ATCAGACAGACCATGATGTGTGTCCAGCTTCAAGAAAGGGGCAAGAGACTCTCTCCAGGCT 709
QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTyrGlyGln 200
Db 710 GACTCGGGGGCCCTGTGTGTGTACAGCTCTTCAAGGCAATATCTCTCGGGGGCCAG 769
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OY 201 ASPROCYSALAIIEThrArglysProGlyValIYrThrIysValCylslyTYrValasp 220
 DB 770 GATCGGTGTCATCACCAGAAAGCTGTGTCTACACGAAAGTCTGCAAAATATGTGAC 829
 OY 221 TRPIEGINGluThMeTlysasn 229
 DB 830 TCGATCCAGACACATGAGAACAAAT 856
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 AC AAA37072;
 XX 08-AUG-2000 (first entry)
 DT
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 XX
 KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
 KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening;
 ss.
 XX Homo sapiens.
 OS
 XX
 PN WO200012708-A2.
 PD 09-MAR-2000.
 XX
 PF 01-SEP-1999; 99WO-US20111.
 XX
 PR 01-SEP-1998; 98US-0098716.
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 PR 01-SEP-1998; 98US-0098750.
 PR 02-SEP-1998; 98US-0098803.
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 PR 09-SEP-1998; 98US-0098596.
 PR 09-SEP-1998; 98US-0098598.
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 PR 03-NOV-1998; 98US-0106856.
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 PR 18-NOV-1998; 98US-0108848.

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PR 18-NOV-1998; 98US-0108849.
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PR 18-NOV-1998; 98US-0108852.
PR 18-NOV-1998; 98US-0108853.
PR 18-NOV-1998; 98US-0108854.
PR 18-NOV-1998; 98US-0108904.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
XX WPI, 2000-237871/20.
XX P-PSDB; AAY93390.
XX
XX New mammalian DNA sequences encoding transmembrane, receptor or
XX secreted PRO polypeptides, useful for screening of potential peptide or
XX small molecule inhibitors of the relevant receptor/ligand interactions
XX
XX Claim 2; Fig 101; 773pp; English.
XX
XX - AAA37022 to AAA37144 encode the new isolated human transmembrane,
XX receptor or secreted PRO polypeptides given in AAY93340 to AAY93462. The
XX transmembrane and receptor PRO proteins can be used for screening of
XX potential peptide or small molecule inhibitors of the relevant
XX receptor/ligand interactions. The polypeptides and nucleotide sequences
XX encoding them have various industrial applications, including uses as
XX pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent
XX PCR primers and hybridisation probes used in the isolation of the PRO
XX polypeptides from the present invention.
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Alignment Scores:
Pred. No.: 5.04e-105 Length: 1204
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
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Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

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Db 289 CACTGCTTAAGCCCGCTACATAGTTCACCTGGGGCAGACACAACTCCAGAGGGAGG 348
QY 61 GLYCYSGULGNLTHRARGTHRALATHRGLUSERPHEPROHISPROGLYPHEASNAHSER 80
Db 349 GGCTGGAGACAGACCCGACAGCACTGAGTCTTCCGCCACCCCGGCTTCAACAACAGC 408
QY 81 leuproaenlyasphlsarghsanaepjlemtleuvallyswelaaserprovalser 100
Db 409 CTCGCCCAACAAAGACACCGCAATGATCATGCTGTAAGTGGCATCGCCAGCTCC 468
QY 101 llettrtralaValArgproleuthrleuserSerArgCysValThrAlaGlyThrSer 120
Db 469 ATCACCCTGGGCTGTGGACCCCTCACTCTCTCTCACTGCTGTGATGCTGGACACAGC 528
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QY 161 llethrAspThrMetValCysAlaSerValGlnGlnGlyIlyAspSerCysGlnGly 180
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Db 709 GACTCCGGGGGGCCCTCTGCTGTATACAGTCTCTTCAAGGACATTATCTCTGGGCCAG 768
QY 201 AspProCysAlaIleThrArgLysProGlyValTyrrThrLysValCysLysTyrrValAsp 220
Db 769 GATCCGCTGTGCATCACCCGAAAGCCTGGTGTCTACACGAAAGTGTGCAAAATGTGAGAC 828
QY 221 TrpIleGlnGlyThrMetLysAsn 229
Db 829 TGCATCCAGAGACGATGAAGAAAT 855

RESULT 7
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ID AAS21496 strand; cDNA; 1204 BP.
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XX AAS21496;
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XX 24-OCT-2001 (first entry)
XX
XX DE Human cDNA sequence encoding for PRO1279 polypeptide.
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XX KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;
XX breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
XX cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
XX adipocyte; A-peptide; factor VIIA; gene therapy; se.
XX
XX OS Homo sapiens.
XX
XX PN WO200140466-A2.
XX
XX PD 07-JUN-2001.
XX
XX PF 01-DEC-2000; 2000WO-US32678.
XX
XX 01-DEC-1999; 99WO-US28301.
XX 01-DEC-1999; 99WO-US28634.
XX 02-DEC-1999; 99WO-US28551.
XX 02-DEC-1999; 99WO-US28564.
XX 02-DEC-1999; 99WO-US28565.
XX 09-DEC-1999; 99US-0170262.
XX 16-DEC-1999; 99WO-US30095.
XX 20-DEC-1999; 99WO-US30911.
XX 20-DEC-1999; 99WO-US30999.
XX 30-DEC-1999; 99WO-US31243.
XX 06-JAN-2000; 2000WO-US00277.
XX 06-JAN-2000; 2000WO-US00376.
XX 11-FEB-2000; 2000WO-US00365.
XX 18-FEB-2000; 2000WO-US04341.
XX 18-FEB-2000; 2000WO-US04342.
XX 22-FEB-2000; 2000WO-US04414.
XX 24-FEB-2000; 2000WO-US04914.
XX 24-FEB-2000; 2000WO-US05004.
XX 24-FEB-2000; 2000WO-US05004.
XX 01-MAR-2000; 2000WO-US05601.
XX 20-MAR-2000; 2000WO-US07377.
XX 21-MAR-2000; 2000WO-US07532.
XX 30-MAR-2000; 2000WO-US08439.
XX 17-MAY-2000; 2000WO-US13705.
XX 22-MAY-2000; 2000WO-US14042.
XX 30-MAY-2000; 2000WO-US14941.
XX 02-JUN-2000; 2000WO-US15264.
XX 10-NOV-2000; 2000WO-US30873.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W,
XX Geritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S,
XX Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

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XX WPI: 2001-408281/43.
 DR P-PSDB; AAU12424.
 XX Isolated, secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing
 PT other PRO polypeptides, and detect the presence of mammalian tumours e.g.
 PT lung, breast, prostate, cervical
 PS Claim 3; Fig 505; 813bp; English.
 XX
 CC AAS21244-AAS21518 encode for novel human secretory and transmembrane
 CC PRO polypeptides. The PRO polypeptides are useful to detect other
 CC PRO polypeptides, to link bioactive molecules to cells expressing
 CC PRO polypeptides, to modulate biological activities of cells expressing
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample.
 CC Some of the 275 sequences are also useful to stimulate the release of
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
 CC proliferation or differentiation of chondrocytes, the proliferation or
 CC gene expression in pericyte cells, the release of proteoglycans from
 CC cartilage, the proliferation of inner ear utricular supporting cells or
 CC of T-lymphocytes, the release of a cytokine from peripheral blood
 CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
 CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
 CC to factor VIIa. The PRO polypeptides can be used in assays to identify
 CC molecules involved in binding interactions. The polynucleotides encoding
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy.
 XX
 SQ Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;
 XX
 Alignment Scores:
 Pred. No.: 5 04e-105 Length: 1204
 Score: 1258.00 Matches: 229
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0
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 DB 169 ATCATCAAGAGGGTTGAGTGAAGAGCTCCTCCAGCCCTTGACAGACCCCTGTTGAG 228
 QY 21 lvsftrhrgleuleucysglyalathrleuilealaiproartryrleuleuthralaala 40
 DB 229 AAGAGCGCGCTACTCTGTGGGGCGAGCGCTCATCGCCCAAGATGGCTCTGACACAGCC 288
 QY 41 Hiscysleuylslyprartryrilevalhslenglyglnhisasnleuglnlysglugu 60
 DB 289 CACTGCTTAAGCCCGGCTACATAGTTTCACTGGGGACACACAACCTCCAGAGAGGAG 348
 QY 61 glycysgluglnthrargrthralathrgluserpheprohisproglypheasnaanser 80
 DB 349 GGCTGTGAGCAGACCCGAGCAGCACTGAGTCTTCCCAACCCGGGCTTCAACAACAGC 408
 QY 81 leuproasnlyasphisarasnaspillemetleuvallysmetallaserprovaliser 100
 DB 409 CTCCCCAACAAGACACCGCAGCATATCATGTGTGATGATGATGATGATGATGATGATG 468
 QY 101 llettrtralaivalarproleuthrleuserserargcyvalthralaglythrser 120
 DB 469 ATCACTGGGCTGTGGACCTTCACTCTCTCACTGATGATGATGATGATGATGATGATG 528
 QY 121 cysleuileserglytyrpolysertthrserserproglinleuargleuprohisthrleu 140
 DB 529 TGCCATATTTCGGGCTGGGAGCAGGTCCACCCCAAGTTACGGCTGCTCAACACCTTG 588
 QY 141 ArgCysAlaAsnIleThrIleIleGIuHisGlnlyCysGluAsnAlaTyrProGlyAsn 160

DB 589 CGATGCGGCAACATCATCATATTGAGCAGCAGAGTGTGAAACGCTTACCCCGGCAC 648
 QY 161 llethraepthrmecvalcysalaservalglnuglylyspaspserycysglnly 180
 DB 649 ATCAGACACACATAGTGTGTGCGCAGCTGCAAGAGGGGCAAGACTCTTCCAGGGT 708
 QY 181 aspseryglytyrproleuvalcysasnlnserleuglnlylleisertryglyln 200
 DB 709 GACTCCGGGGCCCTCTGGTCTGTATACACAGTCTCTCAAGGCAATATCTCTGGGGCCAG 768
 QY 201 aspprocyalailethrarlysparglyvaltyrthrlyvalcyslystlyvalasp 220
 DB 769 GATCGGTGTGATCACCCGAAAGCCGTGTCTTACAGAAAGTCTGCAATATGTGAC 828
 QY 221 trylleglnlgnthrmeclyasasn 229
 DB 829 TGGATCCAGAGACGATTAAGACAAAT 855
 RESULT 8
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 ID AAF54320 standard; DNA; 1204 BP.
 XX
 AC AAF54320;
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 DT 02-APR-2001 (first entry)
 XX
 DE DNA encoding protein of the invention #51.
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 KW Secreted; transmembrane; gene therapy; ss.
 XX
 OS Unidentified.
 OS
 PN WO200078961-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 18-FEB-2000; 2000WO-US04342.
 XX
 PR 23-JUN-1999; 99US-0141037.
 XX
 PR 20-JUL-1999; 99US-0144758.
 XX
 PR 26-JUL-1999; 99US-0145698.
 XX
 PR 01-SEP-1999; 99WO-US20111.
 XX
 PR 29-OCT-1999; 99US-0162506.
 XX
 PR 30-NOV-1999; 99WO-US28313.
 XX
 PR 02-DEC-1999; 99WO-US28551.
 XX
 PR 16-DEC-1999; 99WO-US30095.
 XX
 PR 05-JAN-2000; 2000WO-US00219.
 XX
 PR 06-JAN-2000; 2000WO-US00376.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S,
 PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ,
 PI Pan J, Peoni NF, Roy MA, Smith V, Gurney TA, Tumas D,
 PI Watanabe CK, Williams PM, Wood WI;
 XX
 DR WPI: 2001-071395/08.
 XX
 PT Secreted and transmembrane proteins and nucleic acids designated PRO,
 PT useful as hybridization probes, in chromosome and gene mapping and gene
 PT therapy -
 PS Claim 2; Fig 101; 787bp; English.
 XX
 CC The present invention relates to secreted and transmembrane proteins.
 CC These proteins and the DNA encoding them may be used as hybridization
 CC probes, in chromosome and gene mapping and in the generation of
 CC anti-sense RNA and DNA. They may also be used to generate either
 CC transgenic animals or knockout animals which are in turn useful for
 CC development and screening of therapeutically useful reagents.
 CC The nucleic acids may also be used in gene therapy.
 XX

Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
5.04e-105	1258.00	100.00%	100.00%	100.00%	1204	229	0	0	0	0

US-09-856-320a-2_COPY_54_282 (1-229) x AAF54320 (1-1204)

```

QY      1  llellelygglPheglucysylsProHisserGlnProtrpGlnAlaAlaLeupheglu 20
DB      169 ATCATCAAGGGGTTCCAGTGCAGAGCTCACTCCACGCCGAGGACGCCCTGTTCCAG 228
QY      21  lvsThArgleuleucysglAlaThrLeuIleAlaProArgrTrpleuleuThraAla 40
DB      229 AAGACCCGGCTACTGCTGGGGCGAGCGCTCATCGCCCGCAGATGCTCTCGACAGCAGCC 288
QY      41  HisCysleuLysProArgrTrpIleValHisleuGlyGlnHisasnleuGlnysglu 60
DB      289 CACTGCTCAAGGCCCGCTACATAGTTCACTGGGGGACACAACTCCAGAGGAGGAG 348
QY      61  GlyCysgluGlnThrArgrThraIaThrGlySerPheProHisProglYpheaNaenser 80
DB      349 GGGTGGACAGACGCCGGACAGCAGCTAGTCTTCCCGCCCGGCTTCAACAAACAGC 408
QY      81  LeuproAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
DB      409 CTCGCCAAGAAAGACACCGCAATGACATCATCTGTAAGATGAGCATCGCCAGTCTCC 468
QY      101  lleThTrAlaValArpProleuThrLysSerArGysValThrIaGlyThrSer 120
DB      469 ATCACTGGAGCTGTGGACCCCTCCTCTCTCAAGCTGTGTCACTGTGACCTGACACAGC 528
QY      121  CysLeuIleSerGlyTrpGlySerThrSerSerProGlnleuArpLeuProHisThrLeu 140
DB      529 TGCCTATTTCCGGCTGGGGGACAGCTCAAGCCCACTTACGCTTACACACCTTG 588
QY      141  ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTyProGlyAsn 160
DB      589 CGATGGCCCAACATCACTCATTCATGAGCACCAAGATGAGAGACCTACACCCGGCAAC 648
QY      161  lleThAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGlnGly 180
DB      649 ATCAACAGACCATGGTGTGTGTCAGCGTGCAGGAAGGGGAGGAGACCTCCGACGGGT 708
QY      181  AspSerGlyGlyProleuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200
DB      709 GACTCCGGGGGCCCTCTGGTCTGTATACAGTCTCTTCAAGGCAATTATCTCTGGGGCCAG 768
QY      201  AspProCysAlaIleThrArgrLysProGlyValTyThrLysValCysLysTyValAsp 220
DB      769 GATCCGCTGGCGATCAACCGAAAGCTGTGTCTACACAAAGTGTGCAAAATATATGAGAC 828
QY      221  TrpIleGlnGlyThrMetLysAsnAsn 229
DB      829 TGGATTCAGAGACGATGAAGAACAT 855

```

RESULT 9

ABL95664
ID ABL95664 standard; cDNA; 1204 BP.

XX ABL95664;

XX 19-JUL-2002 (first entry)

DE Human angiogenesis related cDNA PRO1279 SEQ ID NO: 207.

XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
 KW cardiant; cyostatic; antiangiogenic; hypotensive; vulnerability;

```

KW      antiarteriosclerotic; gene; ss.
XX
XX      Homo sapiens.
XX      WO200208284-A2.
XX
XX      31-JAN-2002.
XX
XX      09-JUL-2001; 2001WO-US21735.
XX
XX      20-JUL-2000; 2000US-219556P.
XX      25-JUL-2000; 2000US-220624P.
XX      25-JUL-2000; 2000US-220664P.
XX      28-JUL-2000; 2000WO-US20710.
XX      02-AUG-2000; 2000US-222959P.
XX      17-AUG-2000; 2000US-0643657.
XX      23-AUG-2000; 2000WO-US23522.
XX      24-AUG-2000; 2000WO-US23328.
XX      07-SEP-2000; 2000US-230978P.
XX      15-SEP-2000; 2000US-000000P.
XX      18-SEP-2000; 2000US-0664610.
XX      18-SEP-2000; 2000US-0665350.
XX      24-OCT-2000; 2000US-242922P.
XX      08-NOV-2000; 2000US-0709238.
XX      08-NOV-2000; 2000WO-US30952.
XX      10-NOV-2000; 2000WO-US30873.
XX      01-DEC-2000; 2000WO-US32678.
XX      20-DEC-2000; 2000US-0747259.
XX      20-DEC-2000; 2000WO-US34956.
XX      22-JAN-2001; 2001US-0767609.
XX      28-FEB-2001; 2001US-0796498.
XX      28-FEB-2001; 2001WO-US06520.
XX      01-MAR-2001; 2001WO-US06666.
XX      09-MAR-2001; 2001US-0802706.
XX      14-MAR-2001; 2001US-0808689.
XX      22-MAR-2001; 2001US-0816744.
XX      05-APR-2001; 2001US-0828366.
XX      10-MAY-2001; 2001US-0854208.
XX      10-MAY-2001; 2001US-0854280.
XX      25-MAY-2001; 2001US-0866028.
XX      25-MAY-2001; 2001US-0866034.
XX      25-MAY-2001; 2001WO-US17092.
XX      30-MAY-2001; 2001US-0870574.
XX      30-MAY-2001; 2001WO-US17443.
XX      01-JUN-2001; 2001WO-US17800.
XX      20-JUN-2001; 2001WO-US19692.
XX      28-JUN-2001; 2001WO-US00000.
XX
XX      (GETH ) GENENTECH INC.
XX      (BAKE/) BAKER K P.
XX      (FERR/) FERRARA N.
XX      (GERB/) GERBER H.
XX      (GERR/) GERRITSEN M E.
XX      (GODD/) GODDARD A.
XX      (GODO/) GODOWSKI P J.
XX      (GURN/) GURNEY A L.
XX      (HILL/) HILLAN K J.
XX      (MARS/) MARSTERS S A.
XX      (PANJ/) PAN J.
XX      (PAON/) PAONI N F.
XX      (STEP/) STEPHAN J F.
XX      (WATR/) WATANABE C K.
XX      (WILL/) WILLIAMS P W.
XX      (WOOD/) WOOD W I.
XX
XX      Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
XX      Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
XX      Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX      WPI; 2002-171999/22.
XX      P-PSDB; ABB95526.
XX
XX      One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT

```

PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal -

XX Claim 1, Fig 207; 567bp; English.

CC The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarction, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a coding sequence of the invention.

XX SQ Sequence 1204 BP; 306 A; 364 C; 234 G; 240 T; 0 other;

Alignment Scores:

Pred. No.:	5, 04e-105	Length:	1204
Score:	1258.00	Matches:	229
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-09-856-320a-2_copy_54_282 (1-229) x ABL95664 (1-1204)

QY 1 llelelysglyphneicyslyspromissserpinprotrpinaiaaleuphegiu 20
DB 169 ATCATCAAGGGGTTGAGTGAAGAGCTCCTCCAGCCTTGACAGCACTGTTGAG 228
QY 21 lyeThrAngLeuLeuCyseGlyAlaThrLeuIleAlaProArTrpLeuLeuThrAla 40
DB 229 AAGAGCGCGCTACTGTGGGCGAGCGCTCATCGCCCAAGATGCTCTCTGACACAGCG 288
QY 41 HsCysLeuLysProArTrpYrileValHsLeuGlyGlnHsAsnLeuGlnysGlnu 60
DB 289 CACTGCTCAAGCCCGCTACATAGTTCACTGGGGACACCACTCCAGAGAGAG 348
QY 61 GlyCyseGlnGlnThrArGThrAlaThrGlyserPheProHsProGlyPheAsnAsnSer 80
DB 349 GGCTGTGACAGACCCGAGACGACGACTGAGTCTTCCCAACCCGGCTTCAACAACAGC 408
QY 81 leuproAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
DB 409 CTCCTCCAAACAAAGACCCGCAATGATCATGCTGTGTAAAGATGGCATCGCCAGTCTCC 468
QY 101 ileThrTrpAlaValArpProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
DB 469 ATCACTGGGCTGTGTGACCTCTCCTCCTACGCTGTGTACTGTGACCTGACACG 528
QY 121 CysLeuIleSerGlyTrpGlySerThrSerSerProGlnLeuArgLeuProHsThrLeu 140
DB 529 TCCCTCATTTCCGGCTGGGGAGACAGTCACCCCAAGTTACGCTGCTCACACCTTG 588
QY 141 ArgCysAlaAsnIleThrIleIleGlnHsGlnLysCysGlnAsnAlaTyProGlyAsn 160
DB 589 CGATGGCCCAACATCATCATATGAGCCAGAGAGTGAAGAGCCCTACCCCGCAAC 648
QY 161 ileThrAspThrMetValCysAlaSerValGlnGlnGlyLysAspSerCysGlnGly 180
DB 649 ATCAAGACACCATGTGTGTCCAGCGTGCAGAGAGGGGCAAGAGCTCTGCCAGGGT 708
QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200
DB 709 GACTCGGGGGGCTCTGTGTGTACACGCTCTTCAAGGATATATCTCTGGGGCAG 768
QY 201 AspProCysAlaIleThrArGlySerProGlyValIlyrThrValCysAlaGlyrValAsp 220
DB 769 GATCGGTGTGCATACCCGAAAGCTGTGTCTACAGAAAGTCTGCAAAATATGTGAC 828
QY 221 TrpIleGlnGlnuThrMetLysAsnAsn 229
DB 829 TGGATCCAGAGACGATGAAGAACAT 855

RESULT 10
ABL88175
ID ABL88175 standard; cDNA; 1204 BP.

XX ABL88175;

XX 16-MAY-2002 (first entry)

DE Human PRO1279 cDNA sequence SEQ ID NO:207.

KW Human; angiogenesis; cardiac; cytoskeletal; antiangiogenic; hypotensive;
KW vulnerable; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KW age-related macular degeneration; arterial restenosis; angina;
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KW wound healing; chromosome mapping; gene mapping; gene; ss.

OS Homo sapiens.

PN WO200206930-A2.

XX 03-JAN-2002.

XX 20-JUN-2001; 2001WO-US19692.

XX 23-JUN-2000; 2000US-213637P.

XX 20-JUL-2000; 2000US-219556P.

XX 25-JUL-2000; 2000US-220624P.

XX 25-JUL-2000; 2000US-220664P.

XX 28-JUL-2000; 2000WO-US20710.

XX 02-AUG-2000; 2000US-222695P.

XX 17-AUG-2000; 2000US-064365P.

XX 23-AUG-2000; 2000WO-US23352.

XX 24-AUG-2000; 2000WO-US23328.

XX 07-SEP-2000; 2000US-23078P.

XX 18-SEP-2000; 2000US-0664610.

XX 18-SEP-2000; 2000US-0665350.

XX 24-OCT-2000; 2000US-249222P.

XX 08-NOV-2000; 2000US-070923P.

XX 08-NOV-2000; 2000WO-US30952.

XX 10-NOV-2000; 2000WO-US30873.

XX 01-DEC-2000; 2000WO-US32678.

XX 20-DEC-2000; 2000US-0747259.

XX 20-DEC-2000; 2000WO-US34956.

XX 22-JAN-2001; 2001US-0767609.

XX 28-FEB-2001; 2001US-0796498.

XX 28-FEB-2001; 2001WO-US06520.

XX 01-MAR-2001; 2001WO-US06666.

XX 09-MAR-2001; 2001US-0802706.

XX 14-MAR-2001; 2001US-0808689.

XX 22-MAR-2001; 2001US-0816744.

XX 05-APR-2001; 2001US-0828366.

XX 10-MAY-2001; 2001US-0854208.

XX 10-MAY-2001; 2001US-0854280.

XX 25-MAY-2001; 2001US-0866028.

XX 25-MAY-2001; 2001US-0866034.

XX 25-MAY-2001; 2001WO-US17092.

XX 30-MAY-2001; 2001US-0870574.

XX 30-MAY-2001; 2001WO-US17443.

XX 01-JUN-2001; 2001WO-US17800.

(GETH) GENENTECH INC.

PI Baker KP, Ferrara N, Gerber H, Gertlisen ME, Goddard A;

PI Godowski PJ, Gueney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;

PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

XX WPI; 2002-090516/12.

XX P-PsDB; ABB84920.

PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal -
 XX
 XX
 PS Claim 2; Fig 207; 565pp; English.

CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
 CC ABB85003. The PRO proteins and polynucleotides have cardiant, cyostatic,
 CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
 CC activities, and can be used in gene therapy. The PRO polynucleotides,
 CC proteins, agonists and antagonists are useful for treating or diagnosing
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal,
 CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular
 CC degeneration, atherosclerosis, hypertension, arterial restenosis,
 CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
 CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
 CC carcinoma) and wound healing. The PRO polynucleotides have applications
 CC in molecular biology, including use as hybridisation probes, and in
 CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
 CC probes used in the exemplification of the present invention.

SO Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;

Alignment Scores:
 Pred. No.: 5,04e-105 Length: 1204
 Score: 1258.00 Matches: 229
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x ABL88175 (1-1204)

QY 1 IIEIIILYGLYHEGLUCYSYSPROHISERGLNPROTRPGLNLAALALEUPHEGLU 20
 DB 169 ATCATAAAGGGGTTTCAGTGAAGCAAGCTCACTCCACCCCTGGAGCAACCCCTGTCGAG 228
 QY 21 LVSTHARGLEULEUCYSGLYALATHRLEULEALPROARGTRPLEUETHRALA 40
 DB 229 AAGACCGGCTACTGTGTGGGGGACGCTCATGCCCCCAGATGCTCTTGACAGACGC 288
 QY 41 HISCYLEULYSPROARGTRYILEVALHISLEULYGLNHISANLEULNYSGULGU 60
 DB 289 CACTGGCTCAAGCCCGCTACATAGTTCACTGGGGCAGACCACTCCAGAAAGAGGAG 348
 QY 61 GLYCYSGLUGLINTHRARGTHRALATHRGUSERPHEPROHISPROGLYPHEASNENSER 80
 DB 349 GGCTGTGACGACACCGGACAGCCACTGAGTCTTCCACCCCGCTTCAACACACAC 408
 QY 81 LEUPROASNLYASPHISARGASNAAPILMELEULVALLYSEVALASERPROVALSER 100
 DB 409 CTCCCAACAAAGACACCGCAATGACATGCTGTGTAAGTGCATGCGCAGCTTCC 468
 QY 101 IIEHTRTPALAVALARPPROLEUTHRLEUSERSERARGCYSEVALTHRALAGLYTHRSE 120
 DB 469 ATACCTGGGGCTGTGGACCCCTCACCTCTCTCAAGCTGTGTCACTGTGGACACAC 528
 QY 121 CYSEULLESERGLYTRPGLYSERTHRSERSEPRGGLHLEUARGLEUPROHISTHREU 140
 DB 529 TGCCTCATTTCCGGGCTGGGGGACAGCTCAGCCCCCAGCTTACGCTCCACACCTTG 588
 QY 141 ATGCVSALASNIIEHTRILEIIEGLIHISGLINLYSCYGLASNAALATYRPROGLYAN 160
 DB 589 CCAATGGCCAAACATTCACCATATGACACCAAGATGTGAGAACCCCTTACCCCGCAAC 648
 QY 161 IIEHTRASPETHMEVALCYASLASERVALINGULGLYLYASAPSERCYSGINGLY 180
 DB 649 ATCAACAGACACCATGTGTGTGCGACGTCGAGAAAGGGGAGGACCTCCGCCAGGT 708
 QY 181 AAPSERGLYGLYPROLEUVALCYASANGINSEULEINGLYIIELESERTPGLYGIN 200
 DB 709 GACTCCGGGGGCCCTCTGTGTGTACACGATCTTCAAGGACATATATCTCCGGGGCCAG 768

QY 201 AAPPROCYALALIEHTRARGLYSPROGLYVALTYRTHRYEVALCYSLYSTYRVALAEP 220
 DB 769 GATCCGTGTGCATACCCGAAAGCTGTGTCTACACCAAAAGTCTGCAATATGTGCAC 828
 QY 221 TTPILLEGINGLUETHRLEULYSASNAN 229
 DB 829 TCGATCCAGACGACGATGAAGAACAT 855

RESULT 11
 ID ABL883628 standard; cDNA; 1204 BP.

ABK33628;

08-MAY-2002 (first entry)

CDNA encoding human PRO protein, Seq ID No 185.

Human; secreted protein; PRO; tumour; lung cancer; colon cancer;

breast cancer; prostate tumour; rectal tumour; liver tumour;

pericyte cell proliferation; chondrocyte cell proliferation;

tumour necrosis factor-alpha; gene; ss.

Homo sapiens.

29-JUN-2001; 2001WO-US21066.

20-JUL-2000; 2000US-219556P.

25-JUL-2000; 2000US-220585P.

25-JUL-2000; 2000US-220605P.

25-JUL-2000; 2000US-220607P.

25-JUL-2000; 2000US-220624P.

25-JUL-2000; 2000US-220638P.

25-JUL-2000; 2000US-220664P.

26-JUL-2000; 2000US-220893P.

28-JUL-2000; 2000WO-US20710.

23-AUG-2000; 2000WO-US23522.

14-AUG-2000; 2000WO-US23328.

15-SEP-2000; 2000US-000000P.

10-NOV-2000; 2000WO-US30873.

28-NOV-2000; 2000US-253646P.

01-DEC-2000; 2000WO-US32678.

20-DEC-2000; 2000US-0747259.

20-DEC-2000; 2000WO-US34956.

10-FEB-2001; 2001WO-US06520.

10-MAY-2001; 2001US-0854280.

25-MAY-2001; 2001WO-US17092.

(GENTH) GENENTECH INC.

Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ,
 Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI,
 WPI, 2002-172001/22.
 P-PSDB; AAUB3684.

One hundred and twenty two nucleic acids encoding PRO polypeptides,
 useful for treating a PRO related disorder and for diagnosing tumours
 such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
 tumour or liver tumour -

Claim 2; Figure 185; 359pp; English.

The invention relates to one hundred and twenty two nucleic acids
 encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 encode human secreted proteins. The PRO nucleic acids, polypeptides,
 agonists and antagonists are useful for treating a PRO related disorder.
 The PRO polypeptides are useful for diagnosing tumours, especially lung

CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. The PRO polypeptides are useful for stimulating the
CC proliferation of, or gene expression, in pericyte cells, for stimulating
CC the proliferation or differentiation of chondrocyte cells, for
CC stimulating the release of tumour necrosis factor-alpha from human blood,
CC for stimulating or inhibiting the proliferation of normal human dermal
CC fibroblast cells. The PRO polypeptide may also be used as molecular
CC weight markers and for tissue typing. The PRO nucleic acids have
CC applications in molecular biology, including use as hybridisation probes,
CC and in chromosome and gene mapping. ABK3536-ABK3567 represent human
CC PRO protein coding sequences of the invention.

XX
SQ Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;

Alignment Scores:

Pred. No.:	5,04e-105	Length:	1204
Score:	1258.00	Matches:	229
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-09-856-320A-2_copy_54_282 (1-229) X ABK35628 (1-1204)

```
QY 1 Iletlelysglyphgglucyslysprohisserglnprotrpglnalaleupheglu 20
DB 169 ATCATCAAGGGGTTGAGAGCAAGCCTCACTCCAGCCTTGACAGACCCCTGTTGAG 228
QY 21 LYSTTRARGleuLeuCySGlyAlaThrlleuileAlaProArgTrpLeuThrlAla 40
DB 229 AAGAGCGGGTACTCTGTGGGGCGAGCGCTCATCGCCCAAGATGGCTCTGACAGACGC 288
QY 41 HisCySleuLySProArgTrlIleValHisleuGlyGlnHisAsnleuGlnLySglu 60
DB 289 CACTGCCTCAAGCCCGCTACATAGTTCACTGGGGCAGACACCACTCAGAAAGAGAG 348
QY 61 GlyCySgluGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnSer 80
DB 349 GGCTGTGAGACAGACCCGAGACCCAGCTGCTCTCCCGCCCGCTTCAACACAGC 408
QY 81 LeuProAsnLySAspHisArgAsnAspIleMetLeuVallyMetAlaSerProValSer 100
DB 409 CTCGCCAAGAAAGACCCGCAATGATGATGCTGTAAGATGGCATCGCAGCTTCC 468
QY 101 IletHrTPAlaValArgProleuthrleuSerSerArgCySValThrlaGlyThrSer 120
DB 469 ATCACCTGGGCTGTGGACCCCTCACTCTCTCACTGCTGTCACCTGCGACAGC 528
QY 121 CysleuIleSerGlyTrpGlySerThrSerSerProGlnleuArgleuProHisThrleu 140
DB 529 TCCCTCATTTCCGGGGGAGACAGCTCCACCCCACTTACGCTGCTACACCTTG 588
QY 141 ArgCySAlaAsnIleThrIleleuGlnHisGlnLySAsnAlaTyPProGlyAsn 160
DB 589 CGATGGCCCAATCATCACTTACGACCAAGAGTGTGAAGACCTTACCCCGGAC 648
QY 161 IletHrAspThrMetValCySAlaSerValGlnGlyLySAspSerCySglnGly 180
DB 649 ATCACAGACACCATGGTGTGTGCGCAGCGTGAAGAGGGGCAAGACTCTGCCAGGT 708
QY 181 AspSerGlyGlyProleuValCySAsnGlnSerleuGlnGlyIleIleSerTrpGlyGln 200
DB 709 GACTCGGGGGCCCTCTGTGTGTAAACGCTCTTCAAGGATTAATCTCCGGGCGCAG 768
QY 201 AspProCySAlaIleThrArgLySProGlyValTyThrllyValCySlySlyValAsp 220
DB 769 GATCGGTGTGCGATACCCGAAAGCTGTGTCTACAGAAAGTCTGCAAAATATGTGAC 828
QY 221 TrpIleGlnGluThrMetLySAsnAsn 229
DB 829 TCGATCCAGAGACGATGAAGAAAT 855
RESULT 12
```

```
.ACA03855
ID ACA03855 standard; CDNA: 1204 BP.
AC ACA03855;
XX
XX 23-MAY-2003 (first entry)
DT
XX
XX cDNA encoding human PRO polypeptide #253.
DE
XX
XX Human; PRO polypeptide; secreted and transmembrane protein;
XX tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
XX differentiation; chondrocyte; tumour; genetic disorder;
XX cytoskeletal; gene; ss.
XX
XX Homo sapiens.
XX
XX US2003036180-A1.
XX
XX 20-FEB-2003.
XX
XX 09-MAY-2002; 2002US-0143114.
XX
XX 31-MAR-1997; 97WO-US05230.
XX 12-JUN-1998; 98WO-US12456.
XX 14-JUL-1998; 98WO-US14552.
XX 28-AUG-1998; 98WO-US17888.
XX 10-SEP-1998; 98WO-US18824.
XX 14-SEP-1998; 98WO-US19093.
XX 14-SEP-1998; 98WO-US19094.
XX 14-SEP-1998; 98WO-US19177.
XX 16-SEP-1998; 98WO-US19330.
XX 17-SEP-1998; 98WO-US19437.
XX 07-OCT-1998; 98WO-US21141.
XX 29-OCT-1998; 98WO-US22992.
XX 29-OCT-1998; 98WO-US22992.
XX 20-NOV-1998; 98WO-US24855.
XX 01-DEC-1998; 98WO-US25108.
XX 05-JAN-1999; 99WO-US00106.
XX 08-MAR-1999; 99WO-US05028.
XX 10-MAR-1999; 99WO-US05190.
XX 20-APR-1999; 99WO-US08615.
XX 14-MAY-1999; 99WO-US10733.
XX 02-JUN-1999; 99WO-US12252.
XX 01-SEP-1999; 99WO-US20111.
XX 08-SEP-1999; 99WO-US20594.
XX 13-SEP-1999; 99WO-US20944.
XX 15-SEP-1999; 99WO-US21090.
XX 15-SEP-1999; 99WO-US21547.
XX 05-OCT-1999; 99WO-US23089.
XX 29-NOV-1999; 99WO-US28214.
XX 30-NOV-1999; 99WO-US28313.
XX 30-NOV-1999; 99WO-US28409.
XX 01-DEC-1999; 99WO-US28301.
XX 01-DEC-1999; 99WO-US28634.
XX 02-DEC-1999; 99WO-US28551.
XX 02-DEC-1999; 99WO-US28564.
XX 02-DEC-1999; 99WO-US28565.
XX 16-DEC-1999; 99WO-US30095.
XX 20-DEC-1999; 99WO-US30911.
XX 20-DEC-1999; 99WO-US30999.
XX 22-DEC-1999; 99WO-US30720.
XX 30-DEC-1999; 99WO-US31243.
XX 30-DEC-1999; 99WO-US31274.
XX 05-JAN-2000; 2000WO-US00219.
XX 06-JAN-2000; 2000WO-US00277.
XX 06-JAN-2000; 2000WO-US00376.
XX 11-FEB-2000; 2000WO-US03565.
XX 18-FEB-2000; 2000WO-US04341.
XX 18-FEB-2000; 2000WO-US04342.
XX 22-FEB-2000; 2000WO-US04914.
XX 24-FEB-2000; 2000WO-US04914.
XX 24-FEB-2000; 2000WO-US05004.
XX 01-MAR-2000; 2000WO-US05601.
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02-MAR-2000; 2000MO-US05746.
 02-MAR-2000; 2000MO-US05841.
 10-MAR-2000; 2000MO-US06319.
 15-MAR-2000; 2000MO-US06884.
 20-MAR-2000; 2000MO-US07377.
 21-MAR-2000; 2000MO-US07532.
 30-MAR-2000; 2000MO-US08439.
 17-MAY-2000; 2000MO-US13705.
 22-MAY-2000; 2000MO-US14042.
 30-MAY-2000; 2000MO-US14941.
 02-JUN-2000; 2000MO-US15264.
 28-JUL-2000; 2000MO-US20710.
 11-AUG-2000; 2000MO-US22031.
 23-AUG-2000; 2000MO-US23522.
 08-NOV-2000; 2000MO-US30952.
 10-NOV-2000; 2000MO-US30873.
 01-DEC-2000; 2000MO-US32678.
 20-DEC-2000; 2000MO-US34956.
 28-FEB-2001; 2001MO-US06520.
 01-MAR-2001; 2001MO-US06666.
 25-MAY-2001; 2001MO-US17092.
 01-JUN-2001; 2001MO-US17800.
 20-JUN-2001; 2001MO-US19692.
 22-JUN-2001; 2001MO-US20116.
 29-JUN-2001; 2001MO-US21066.
 09-JUL-2001; 2001MO-US21735.
 20-DEC-2000; 2000MO-US247259.
 28-FEB-2001; 2001MO-US247259.
 09-MAR-2001; 2001MO-US202706.
 14-MAR-2001; 2001MO-US08689.
 22-MAR-2001; 2001MO-US0816744.
 05-APR-2001; 2001MO-US0828366.
 10-MAY-2001; 2001MO-US084208.
 10-MAY-2001; 2001MO-US084280.
 18-MAY-2001; 2001MO-US0860216.
 25-MAY-2001; 2001MO-US0866028.
 01-JUN-2001; 2001MO-US0866034.
 05-JUN-2001; 2001MO-US0872035.
 14-JUN-2001; 2001MO-US0874503.
 19-JUN-2001; 2001MO-US0882636.
 21-JUN-2001; 2001MO-US0886342.
 18-JUL-2001; 2001MO-US0887879.
 06-AUG-2001; 2001MO-US0908827.
 09-AUG-2001; 2001MO-US0924419.
 16-AUG-2001; 2001MO-US0927796.
 19-DEC-2001; 2001MO-US0931836.
 (GENTH) GENENTECH INC.
 Baker KP, Beresini M, DeGeorge L, Desnoyers L, Filvaroff E, Gao W, Gertlisen WE, Goddard A, Godowski PJ, Gurney AL, Sherwood S, Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z, WPI: 2003-332040/31.
 P-PSDB; AB066822.
 New secreted and transmembrane PRO nucleic acids, useful for gene therapy, in chromosome and gene mapping, as chromosome markers, in tissue typing, and in chromosome identification
 Claim 2: Fig 505; 660pp; English.

CC the proliferation or differentiation of chondrocytes, and detecting the
 CC presence of tumours. The polynucleotide sequences encoding PRO
 CC polypeptides are useful as hybridisation probes, in chromosome and
 CC gene mapping, in the generation of antisense RNA and DNA, in the
 CC preparation of PRO polypeptides, for generating transgenic animals or
 CC knockout animals, for the genetic analysis of individuals with genetic
 CC disorders, and in gene therapy. ACA03603-ACA03877 represent cDNAs
 CC encoding the human PRO polypeptides of the invention.
 CC Note: The sequence data for this patent was obtained in electronic
 CC format directly from the USPTO web site at
 CC seqdata.uspto.gov/psipdsidentry.html.
 CC
 XX
 SQ Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;
 Alignment Scores:
 Pred. No.: 5,04e-105 Length: 1204
 Score: 1258.00 Matches: 229
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0
 US-09-856-320A-2_COPY_54_282 (1-229) x ACA03855 (1-1204)
 QY 1 IleIleIysGlyPheGluCysIysProHisSerGlnProTyrGlnAlaAlaLeuPheGlu 20
 DB 169 ATCATCAAGGGGTTGAGTGCAGGCTCACTCCAGCCCTGGCAGGACCCCTGTTCCAG 228
 QY 21 LysThrArgLeuLeuCysGlyAlaThrLeuIleAlaProArgTyrLeuLeuThrAlaAla 40
 DB 229 AAGAGCGGCTACTGTGTGGGGCGAGCGCTCACTCCGCGCAGATGCTCTCGACAGAGC 288
 QY 41 HisCysLeuIysProArgTyrIleValHisIleuGlyGlnHisAsnLeuGlnIysGlu 60
 DB 289 CACTGCTCAAGCCCGCTCACTAGTTCACCTGCGGCGACCAACCTCCAGAGAGAGG 348
 QY 61 GlyCysGlnGlnThrArgThrAlaThrGluSerPheProHisProGlyPheAsnAsnSer 80
 DB 349 GCGTGTGACAGACCCCGAGACCCCACTAGTCTTCCCAACCCCGGCTTCAACACAGC 408
 QY 81 LeuProAsnIysAspHisArgAsnAspIleMetLeuValIysMetAlaSerProValSer 100
 DB 409 CTCGCCAACAAGACACCGCATATCATGTGCTGGAAGATGCATCCGCACTTCC 468
 QY 101 IleThrTPAlaValArgProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120
 DB 469 ATCACTGGGCTGTGCGACCCCTCACTCTCCACCGCTGTGCACGCTGGCAGCAGC 528
 QY 121 CysLeuIleSerGlyTyrGlySerThrSerSerProGlnLeuArgLeuProHisThrLeu 140
 DB 529 TGCTCATTTCCGGCTGGGGGAGCAGCTCCAGCCCGCCAGTTACGCTTCCACACCTTG 588
 QY 141 ArgCysAlaAsnIleThrIleIleGlnHisGlnIysCysGluAsnAlaTyrProGlyAsn 160
 DB 589 CGATCGCCCAATACATCATTTAGAGCAGCAGAGTGTGAAGACCTTACCCCGGCAAC 648
 QY 161 IleThrAspThrMetValCysAlaSerValGlnGluGlyIysAspSerCysGlnGly 180
 DB 649 ATCAGACAGACACATGCTGTGTGCGACGCTGCAGAGAGGGGCAAGACTCTCCGAGGCT 708
 QY 181 AspSerGlyIysProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTyrGln 200
 DB 709 GACTCCGGGGGCTTGT 768
 QY 201 AspProCysAlaIleThrArgIysProGlyValTyrThrIysValCysIysTyrValAsp 220
 DB 769 GATCGGTGTGATGATACCCGAAAGCTGTGTCTTCAACAGAAAGTCTGCAAAATATGTGAC 828
 QY 221 TrpIleGlnGluThrMetIysAsnAsn 229
 DB 829 TGGATCCAGAGACGATGACAGCAAT 855
 RESULT 13

ACA04276
ID ACA04276 standard; cDNA, 1204 BP.
XX
AC ACA04276;
XX
DT 27-MAY-2003 (first entry)
XX
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 505.
XX
KW Human; ss; gene; secreted protein; transmembrane protein; PRO;
KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;
KW infertility; birth defects; premature aging; AIDS; biosensor;
KW acquired immunodeficiency syndrome; cancer; diabetic complication;
KW bioresactor; tumour.
XX
OS Homo sapiens.
XX
PN US2003032155-A1.
XX
PD 13-FEB-2003.
XX
PF 03-MAY-2002; 2002US-0137865.
XX
PR 31-MAR-1997; 97WO-US05230.
PR 12-JUN-1998; 98WO-US12456.
PR 14-JUL-1998; 98WO-US14552.
PR 28-AUG-1998; 98WO-US17888.
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19093.
PR 14-SEP-1998; 98WO-US19094.
PR 14-SEP-1998; 98WO-US19177.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 29-OCT-1998; 98WO-US22991.
PR 29-OCT-1998; 98WO-US22992.
PR 20-NOV-1998; 98WO-US24855.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99WO-US05190.
PR 20-APR-1999; 99WO-US06615.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28409.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 22-DEC-1999; 99WO-US30920.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.

PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05746.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08435.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 22-JUN-2001; 2001WO-US20116.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 20-DEC-2000; 2000US-0747259.
PR 28-FEB-2001; 2001US-0796488.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 18-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 21-JUN-2001; 2001US-0887879.
PR 18-JUL-2001; 2001US-0908827.
PR 06-AUG-2001; 2001US-0924419.
PR 09-AUG-2001; 2001US-0927796.
PR 16-AUG-2001; 2001US-0931836.
PR 19-DEC-2001; 2001US-0028072.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W,
PI Gertsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-331925/31.
DR P-PSDB; ABU67098.
XX
XX New secreted and transmembrane nucleic acids and polypeptides,
PT designated as PRO, useful for treating inflammation, organ failure,
PT atherosclerosis, cardiac injury, infertility, birth defects, premature
PT aging, AIDS, or cancer
XX
XX Claim 2; Fig 505; 659pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising, or which is
CC at least 80% identical to, or the full-length coding sequence of, any of
CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
CC (one of 275 secreted or transmembrane proteins). The nucleic acid
CC further comprises the full-length coding sequence of the DNA deposited
CC under American Type Culture Collection (ATCC) accession number in a list
CC given in the specification. Also included are vectors and host

CC cells for producing PRO proteins, PRO fusion proteins, anti-PRO
CC antibodies, PRO extracellular domains and mature sequences, methods
CC of detecting PRO proteins, methods for stimulating the release of
CC TNF-alpha (tumor necrosis factor alpha) from human blood,
CC (and the proliferation of differentiation of chondrocyte cells, the
CC proliferation of, or gene expression in pericyte cells, the release or
CC proteoglycans from cartilage, proliferation of inner ear utricular
CC supporting cells, the proliferation of T-lymphocyte cells, the release
CC of a cytokine from peripheral blood mononuclear cells (PBMC), or the
CC proliferation of endothelial cells), a method for modulating the uptake
CC of glucose or free fatty acid (FFA) by skeletal muscle cells,
CC a method for inhibiting the binding of A-peptide to factor VIIA,
CC or the differentiation of adipocyte cells, a method for detecting the
CC presence of a tumor in a mammal and an oligonucleotide probe derived
CC from any of the nucleotide sequences cited above. The nucleic acids and
CC polypeptides are useful for treating inflammatory diseases, organ
CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
CC premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or
CC diabetic complications. The nucleic acids are useful as hybridisation
CC probes, in chromosome and gene mapping, and in generating antisense RNA
CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,
CC biosensors or bioreactors. Both are useful in tissue typing.
CC The present sequence encodes a PRO protein of the invention.
XX
SQ Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;

Alignment Scores:

Score: 5.04e-105 Length: 1204
Percent Similarity: 1258.00 Matches: 229
Best Local Similarity: 100.00% Conservative: 0
Query Match: 100.00% Mismatches: 0
DB: Indels: 0
Gaps: 0

US-09-856-320A-2_COPY_54_282 (1-229) x ACA04276 (1-1204)

QY 1 llelellyg1yphelgucyslyspromisserg1nprotropg1nalaaleuphegiu 20
DB 169 ATCATCAAGGGGTTCAGTGCAGCAAGCTCTCCACGCTCGGAGGACGCTGTTCCGAG 228
QY 21 lvsfthArgleuLeuCySG1yalaThrlleu1lea1proArgTrpleuLeuThralaala 40
DB 229 AAGACCCGGCTACTGTGGGGGAGCGCATGATGCCGCCAGATGCTCTGACAGAGC 288
QY 41 HisCyLeuLeuProArgTrpYrlleValHisleuGlyGlnHisAsnleuGlnysgiu 60
DB 289 CACTGCTCAAGCCCGCTACAAAGTTCACTGGGGGACACCAACTCCAGAGGAGGAG 348
QY 61 GlyCyGluGlnThraArgThralaThrgLuserPheProHisSProg1yPheAsnAsner 80
DB 349 GGCTGAGACAGACCCCGACAGCACTGAGTCTTCCCGCCCGGCTTCAACAGAC 408
QY 81 LeuProAsnLysAspHisArgAsnAsp11emetleuVallyseWera1aserProValSer 100
DB 409 CTCGCCCAAGCAAGACACCGCAATGACATGCTGTAAGATGCGATCGCCAGCTCC 468
QY 101 lleThTrpAlaValArgProleuThrlLuserSerArgCyValThralaGlyThrSer 120
DB 469 ATCACTGGGCTGTGGACCCCTCACTCTCTCAAGCTGTGTCACTGTGTCACCTG 528
QY 121 CysLeu1leSerG1yTrpG1ySerThrSerSerProg1nleuArgLeuProHisThrlLeu 140
DB 529 TCCCTCATTTCCGGCTGGGCGAGCAAGTCAAGCCCACTTACGCTGCTCAACACTTG 588
QY 141 ArgCySAlaAsn1leThrlle1leGlnHisGlnLysCySG1yAsnAlaTyRProG1yAsn 160
DB 589 CGATGGCCCAACATCACTCATTTGAGCACCAAGAGTGTGAAGACGCTCAACCCGCAAC 648
QY 161 lleThAspThMerValCysAlaSerValGlnGlyGlyLysAspSerCySG1nGly 180
DB 649 ATCAAGACCAACATGTGTGTGTGCACAGCGGAGGAAGGGGGAAGGACTCCGCCAGGGT 708
QY 181 AspSerG1yG1yProleuValCysaeng1nserLeuGlnGly1le1leSerTrpG1yGln 200

DB 709 GACTCGGGGGCCCTGTGTCTGTACCAAGTCTTCAAGCATATATCTCGGGCCAG 768
QY 201 AppProCySAla1leThraArgLysProG1yVal1TyThrlValAlCysLysTyRValaap 220
DB 769 GATCCGTGTGCATCAACCGAAGCGCTGTGTCTACAGCAAGTCTGCAAAATATGTGAC 828
QY 221 Trp1leGlnG1uThMerLysAsnAsn 229
DB 829 TGGATCCAGAGACGATGAGAACAT 855
RESULT 14
ABX89393
ID ABX89393 standard; cDNA; 1204 BP.
AC ABX89393;
XX
DT 13-MAY-2003 (first entry)
XX
DE DNA encoding novel secreted and transmembrane protein PRO1279.
XX
KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosa; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpeticiforms; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003017563-A1.
XX
PD 23-JAN-2003.
XX
PF 07-MAY-2002; 2002US-0140808.
XX
PR 31-MAR-1997; 97WO-US05230.
PR 12-JUN-1998; 98WO-US12456.
PR 14-JUL-1998; 98WO-US14552.
PR 28-AUG-1998; 98WO-US17888.
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19093.
PR 14-SEP-1998; 98WO-US19094.
PR 14-SEP-1998; 98WO-US19177.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 27-OCT-1998; 98WO-US21141.
PR 29-OCT-1998; 98WO-US22991.
PR 29-OCT-1998; 98WO-US22992.
PR 20-NOV-1998; 98WO-US24855.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99WO-US05190.
PR 20-APR-1999; 99WO-US08615.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28409.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.

PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 22-DEC-1999; 99WO-US30720.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05746.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 22-JUN-2001; 2001WO-US20116.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 20-DEC-2000; 2000US-0747259.
PR 28-FEB-2001; 2001US-0796498.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 18-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001US-0860216.
PR 25-MAY-2001; 2001US-0866028.
PR 01-JUN-2001; 2001US-0865034.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 21-JUN-2001; 2001US-0887879.
PR 18-JUL-2001; 2001US-0908827.
PR 06-AUG-2001; 2001US-0924419.
PR 09-AUG-2001; 2001US-0927796.
PR 16-AUG-2001; 2001US-0931836.
PR 19-DEC-2001; 2001US-0028072.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W,
PI Geriltien ME, Goddard PJ, Gunney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX

DR WPI: 2003-146238/14.
DR P-PBDB: ABU59903.
XX
XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT are therapeutically useful for enhancing immune response and in cancer
PT treatments -
XX
XX Claim 2; Fig 505; 659pp; English.
XX
XX The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC PRO943, PRO828, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumours. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813
CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and
CC are thus useful for treating sports injuries, and arthritis. This
CC sequence encodes a novel human PRO protein.
XX
XX Sequence 1204 BP; 306 A; 364 C; 294 G; 240 T; 0 other;
SQ
Alignment Scores:
Pred. No.: 5.04e-105 Length: 1204
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-09-856-320A-2_COPY_54_282 (1-229) x ABX89393 (1-1204)
QY 1 IleIleIleYsGIYpHeGluCyAlsYsProHisSerGlnProTPrGlnAlaIleuPheGlu 20
Db 169 ATCATCAAGGGGCTTCAGTGAAGCTCACCCTCCAGCCCTGCGACGACCCCTGTCAG 228
QY 21 LysThrArgLeuLeuCyGAlaIleThrIleuIleAlaProArgTPrLeuLeuThrAlaIle 40
Db 229 AAGACGCGGCTACTCTGGGGCGACGCTCATCCGCCCAATGATGCTCTGACGACGCC 288
QY 41 HisCysLeuLysProArgTPrIleValHisIleuLysGlnHisAsnLeuGlnLysGlu 60
Db 289 CACTGCCTCAAGCCCGCTACATGTTCACTGGGGCGACCAACCTCCCAAGGAGAG 348
QY 61 GlyCysGluGlnThrArgThrAlaThrGluSerPheProHisPProGlyPheAsnAsnSer 80
Db 349 GCGTGTGACGACGCCGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 408
QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
Db 409 CTCGCCAACAAGACCAACCGCAATGACATCATCTGTTGAAGATGACATCGCCAGTCTCC 468
QY 101 IleThrTrpAlaValAlaGProLeuThrLeuSerSerArgCysValThrAlaGlyThrSer 120

DB ATCAGCTGGAGTGTGACCCCTCACCCTCTCTCAGCGTGTGTCACTGCTGGCACCAG 528
QY CysLeuIleSerGlyTyrPglYserThrSerSerProGlnLeuArgLeuProHisThrLeu 140
DB 529 TGGCTATTTCGGGCGGAGCAGCAGCTCCAGGCCAGTACGCTGCTCACACCTTG 598
QY ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTyrProGlyAsn 160
DB 589 CGATGGCCCAACTCCATCATTTGAGCCACCAAGGTGAGAACCCCTTACCCCGGCAAC 648
QY 161 IleThrAspThrMetValCysAlaSerValGlnGlnGlyValLysAspSerCysGlnGly 180
DB 649 ATCAGACAGACCATGTGTGTGTCCAGCGTCCAGAAAGGGGGCAAGACTCTCCAGGGT 708
QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTyrGln 200
DB 709 GACTCCGGGGCCCTGTGTGTGTACCACTCTCTTCAAGGCATTTATCTCGGGGCCAG 768
QY 201 AspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTyrValAsp 220
DB 769 GATCCGTGTCCGATTCACCCGAAAGCCTGTGTCTTACACCAAGTCTGCAATATGTGAC 828
QY 221 TrrPleGlnGluThrMetLysAsnAsn 229
DB 829 TGGATCCAGAGACGATGAAGAACAT 855
RESULT 15
ABAB3372
ID ABA83372 standard; cDNA; 1292 BP.
AC ABA83372;
XX
DT 07-FEB-2002 (first entry)
XX
DE Human secreted protein gene 179 SEQ ID NO:189.
XX
XX Human; secreted protein; immunomodulatory; antisclerotic; anti-HIV;
KW dermatological; immunosuppressive; anti-inflammatory; immunostimulant;
KW cytostatic; caldant; vascular; anti-angiogenic; ophthalmological;
KW neuroprotective; nootropic; anticonvulsant; antialzheimer's; vulnary;
KW antiparkinsonian; antimicrobial; gene therapy; vaccine; immune disorder;
KW multiple sclerosis; systemic lupus erythematosus; HIV infection; cancer;
KW human immunodeficiency virus; hyperproliferative disorder; wound healing;
KW Gaucher's disease; cardiovascular disease; Scimitar syndrome; chemotaxis;
KW Chaga's cardiomyopathy; coronary arteriosclerosis; angiogenic disorder;
KW corneal graft neovascularisation; diabetic retinopathy; regeneration;
KW neurological disorder; Huntington's chorea; Alzheimer's disease;
KW Parkinson's disease; infectious disease; ss.
XX
OS Homo sapiens.
XX
PN WO200162891-A2.
XX
PD 30-AUG-2001.
XX
PF 21-FEB-2001; 2001WO-US05614.
XX
PR 24-FEB-2000; 2000US-184836P.
XX
PR 29-MAR-2000; 2000US-193170P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ni J, Ebner R, Lafleur DW, Moore PA, Olsen HS, Rosen CA;
PI Ruben SM, Soppet DR, Young PE, Shi Y, Florence KA, Wei Y;
PI Florence C, Hu J, Li Y, Kyaw H, Fischer CL, Ferris AM, Fan P;
PI Feng P, Endress GA, Dillon PJ, Carter KC, Brewer LA, Yu G;
PI Zeng Z, Greene JM;
XX
DR WPI, 2001-625744/72.
DR P-PSDB; ABB50479.
XX
PT Nucleic acids encoding 207 human secreted polypeptides, useful for

PT preventing, diagnosing and/or treating, e.g. cancers, Parkinson's
XX disease and diabetic retinopathy -
XX
PS Claim 1; Page 1032; 1533pp; English.
XX
XX ABB50301 to ABB51287 and ABA83194 to ABA83441 represent human secreted
CC proteins (I) and polynucleotide (II) sequences. (I) and (II) have various
CC activities based on the tissues and cells the genes are expressed in.
CC Example of these activities include: immunomodulatory; antisclerotic;
CC dermatological; immunosuppressive; anti-inflammatory; immunostimulant;
CC anti-HIV; cytostatic; caldant; anti-angiogenic; ophthalmological;
CC neuroprotective; nootropic; anticonvulsant; antialzheimer's; vascular;
CC antiparkinsonian; antimicrobial; and vulnary. (I) and (II) can be used
CC in gene therapy and vaccine production. (I) and (II) can be used in the
CC prevention, diagnosis and treatment of immune disorders (e.g. multiple
CC sclerosis, systemic lupus erythematosus and human immunodeficiency virus
CC (HIV) infections), hyperproliferative disorders (e.g. cancers and
CC Gaucher's disease), cardiovascular diseases (e.g. Scimitar syndrome,
CC Chaga's cardiomyopathy and coronary arteriosclerosis) and diabetic
CC disorders (e.g. corneal graft neovascularisation and diabetic
CC retinopathy), neurological disorders (e.g. Huntington's chorea,
CC Alzheimer's disease and Parkinson's disease), infectious diseases and/or
CC for promoting wound healing, regeneration and/or chemotaxis. ABA83185 to
CC ABA83193 and ABB50300 represent sequences used in the exemplification of
CC the present invention.
XX
SQ Sequence 1292 BP; 319 A; 387 C; 329 G; 253 T; 4 other;
XX
Alignment Scores:
Pred. No.: 5,52e-105 Length: 1292
Score: 1258.00 Matches: 229
Percent Similarity: 100.00% Conserved: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-09-856-320A-2_COPY_54_282 (1-229) x ABA83372 (1-1292)
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DB 270 ATCATCAAGGGGTTGAGAGCAAGCCTCACCTCCAGCCCTGGCAGACCCCTGTCGAG 329
QY 21 LysThrArgLysLeuCysGlyValaThrLeuIleAlaProArgTrrPleuThrAla 40
DB 330 AAGACGGGCTTCTGTGGGGCGACGCTCATGCCCCCAGATGGCTCTGACAGCAGCC 389
QY 41 HisCysLeuLysProArgTrrIleValHisLeuGlyGlnHisAsnLeuGlnLysGlnGlu 60
DB 390 CACTGCTCAAGCCCGGCTACCTAGTTCACCTGGGGGACACCACTCCAGAAAGAGGAG 449
QY 61 GlyCysGlnGlnThrArgThrAlaThrGlnSerPheProHisProGlyPheAsnAsnSer 80
DB 450 GGCTGTGAGACACCGGACAGCCACTGAGTCTTCCCAACCCCGGCTTCAACACAC 509
QY 81 LeuProAsnLysAspHisArgAsnAspIleMetLeuValLysMetAlaSerProValSer 100
DB 510 CTCCCAACAAAGACACCGGACATGATGATGATGATGATGATGATGATGATGATGATG 569
QY 101 IleThrTrrPalaValaArgProLeuThrLeuSerSerArgCysValIleThrAlaGlyThrSer 120
DB 570 ATCAGCTGGGCGTGTGCAACCCCTCACCTCTCTCAACCTGTGTCACTGCTGGCAGCAGC 629
QY 121 CysLeuIleSerGlyTrrPglYserThrSerSerProGlnLeuArgLeuProHisThrLeu 140
DB 630 TGYCTCATTTCCGGCTGGGGGAGCAGCGTCCAGCCCGGAGTTACGCTGCTCACACCTTG 689
QY 141 ArgCysAlaAsnIleThrIleIleGlnHisGlnLysCysGlnAsnAlaTyrProGlyAsn 160
DB 690 CGATGGCCCAACTCCATCATTTGAGCCACCAAGGTGAGAACCCCTTACCCCGGCAAC 749
QY 161 IleThrAspThrMetValCysAlaSerValGlnGlnGlyValLysAspSerCysGlnGly 180
DB 750 ATCAGACAGACCATGTGTGTGTCCAGCGTCCAGAAAGGGGGCAAGACTCTCCAGGGGT 809

QY 181 AspSerGlyGlyProLeuValCysAsnGlnSerLeuGlnGlyIleIleSerTrpGlyGln 200
 Db 810 GACTCCGGGGGCCCTCTGCTGTGTAAACCACTCTTCAAGCATTAATCTCTGGGGCCAG 869
 QY 201 AspProCysAlaIleThrArgLysProGlyValIleThrLysValCysLysTyrValAsp 220
 Db 870 GATCCGTGTGCAATCACCCGAAAGCCTGTGTGTCTACACGAAGTCTGCNAATATGTGTGAC 929
 QY 221 TrpIleGlnGluThrMetLysAsnAsn 229
 Db 930 TCGATCCAGAGACGATGAAGAACAAT 956

Search completed: October 23, 2003, 15:58:15
 Job time : 260.855 secs

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PROSITE

Proteomics tools

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Handwritten notes:
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6075136
side2
hope-pro-site

Sequence:

MÖRLRWLRDM KSSGRGLTAA KPGARSSPL QAMRIQLLIL LALATGLVGG ETRIIKGFEC
KPHSQPWQAA LFEKTRLLCG ATLIAPRWLL TAAHCLKPRY IVHLGQHNLO KEEGCEQTRT
ATESFPHBGF NNSLPNKDHR NDIMLVKMAS PVSITWAVRP LTLSSRCVTA GTSCGISGWG
STSSPQLRLP HTLRCANITL IEHQKCEENAY PGNITDTMVC ASVQEGGKDS CQGDSSGGPLV
CNGSLQGIS WGDPCAITR KPGVYTKVCK YVDWIDQETMK NN

PROSITE Release 18.10, of 12-Oct-2003

>PDOC00001 ASN_GLYCOSYLATION N-glycosylation site [pattern] [Warning: pattern with a high probability of occurrence].

131 - 134 NNSL
197 - 200 NITI
213 - 216 NITD
242 - 245 NQSL

>PDOC00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site [pattern] [Warning: pattern with a high probability of occurrence].

13 - 15 SGR
164 - 166 SSR
192 - 194 TIR
259 - 261 TRK
278 - 280 Tmk

>PDOC00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site [pattern] [Warning: pattern with a high probability of occurrence].

120 - 123 TAT
199 - 202 TIE
222 - 225 SVQE

>PDOC00008 MYRISTYL_N-myristoylation site [pattern] [Warning: pattern with a high probability of occurrence].

16 - 21 GLTAK
46 - 51 GLVGE
114 - 119 GCEQTR
226 - 231 GSKDSC
252 - 257 GQDPCA

>PDOC00124 PS50240 TRYPSIN_DOM Serine proteases, trypsin domain [profile].

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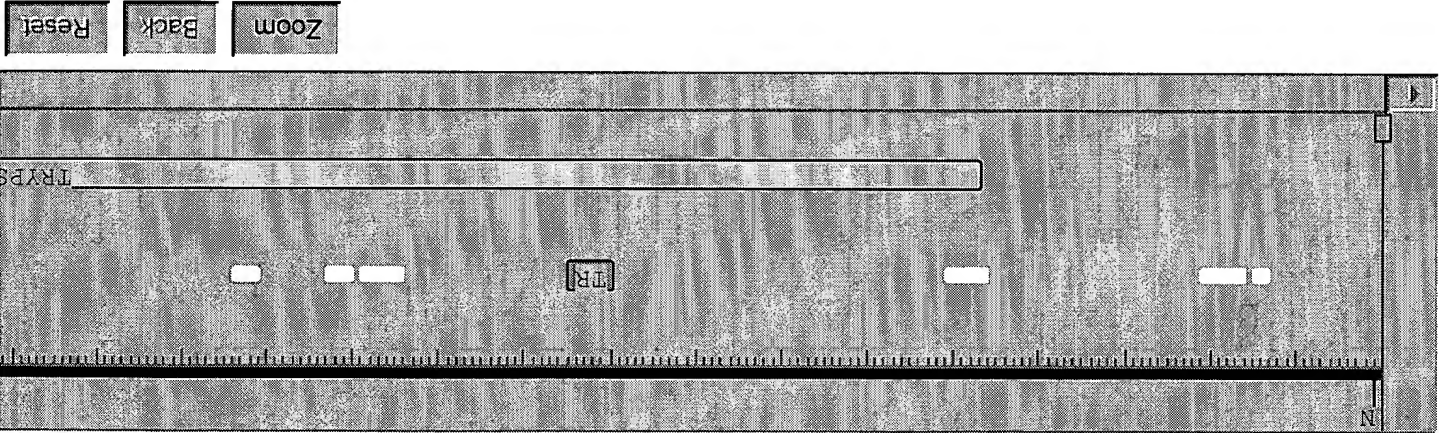
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47 - 280 LVGGEtrikgfECKPHSQPWQALFEKT-RLTCGATLIAPRWLLTAAHCLKPR-----Y
IVHLGQHNLQKEEGCEQTRTATESFPHPGFNslpNKDHRNDIMLVKMASPVSITWAVRP
LTL--SSRCVTAGTSCLSISGWGSTSSPqLRLPHHTLRCANITIIIEHQKC-ENAYPGNITDT
MVCASVQEGGKDSGQDSCQDSSGGPLVC-----NQSLQGIISWGqDPCAITRKPGVYTKVCKKYVD
WIOETMK
```

>PD0C00124 PS00134 TRYPsin_HIS Serine proteases, trypsin family, histidine active site [pattern].
90 - 95 LTAHAC

>PD0C00124 PS00135 TRYPsin_SER Serine proteases, trypsin family, serine active site [pattern].
229 - 240 DScqGDSGGPLV

Graphical summary of hits (java applet)

Click on items to see a description. Drag the two red cursors to select a zoom region.



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